

STIC-Biotech/ChemLib

66305

From: Prouty, Rebecca
Sent: Thursday, May 09, 2002 8:07 AM
To: STIC-Biotech/ChemLib
Subject: Sequence Search

Art Unit 1652, 10A13
Mailbox: 10C01
308-4000
Serial Number: 09/582,397

Please search and interference search SEQ ID NOS: 1-4

CRFE

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1.6A05 308-4291

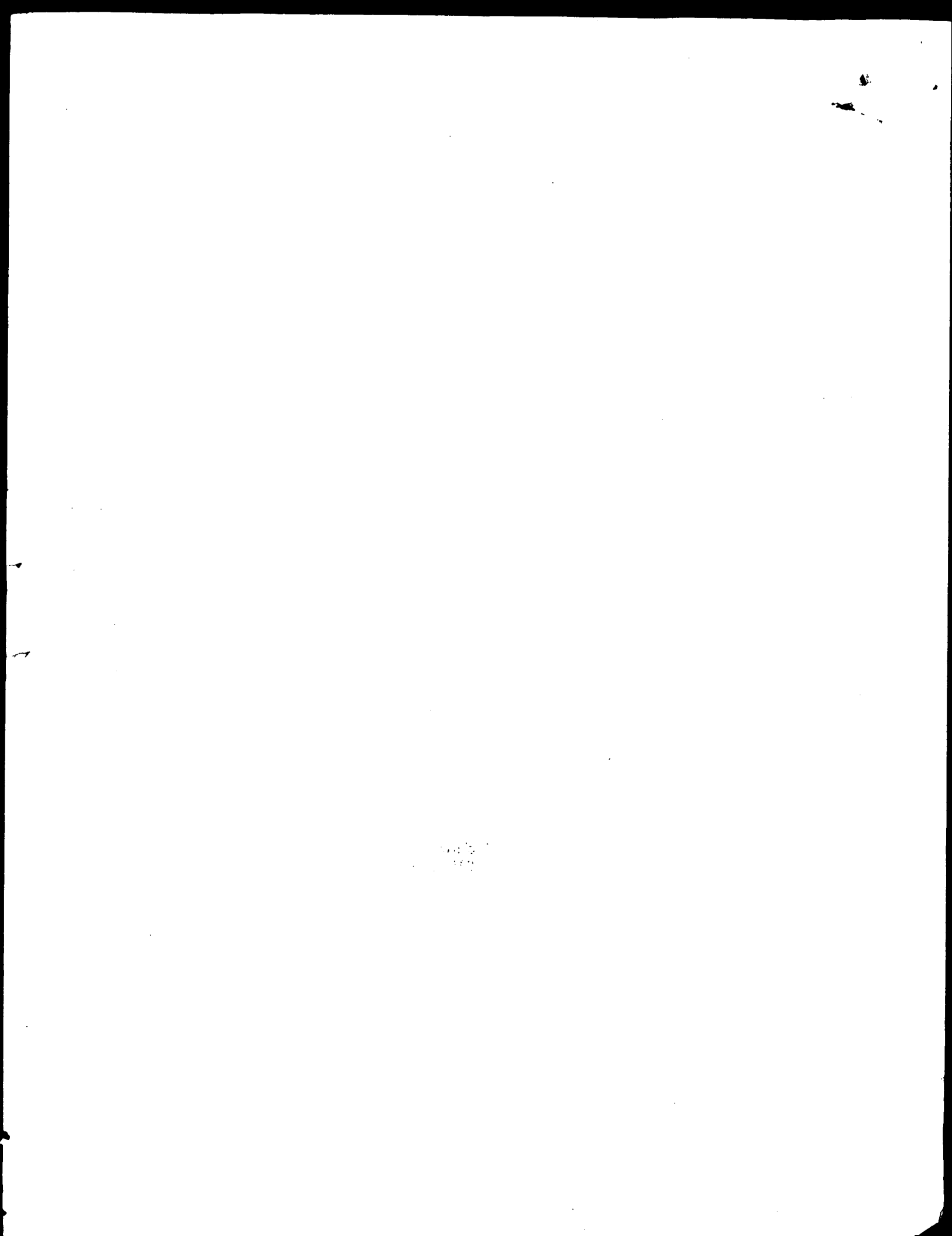
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Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 5-15-02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
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Sequence Sys.: _____
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Other (specify): _____



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2002, 12:08:07 ; Search time 8970.87 Seconds

(Without alignments)
5024.681 Million cell updates/sec

Title: US-09-582-397A-1

Sequence: 1 agatgcagagcagcagcgaat.....agcactcctgagtctgag 2154

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

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32: em_htg_other: *
33: em_htg_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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Result No.	Query Match	Score	Length	ID	Description
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4	2149.4	99.8	2151	9	AF241789 Homo sapi
5	1506.2	69.9	2893	10	AB016589 Mus muscu
6	555.2	25.8	2750	10	AF191839 Mus muscu
7	553.6	25.7	2201	10	AF145705 Mus muscu
8	463.4	21.5	2827	9	AF191838 Homo sapi
9	463.4	21.5	2994	6	AR016417 Sequence
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ALIGNMENTS

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DEFINITION Homo sapiens IKK-1 mRNA for inducible IkappaB kinase, complete cds.
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VERSION AB016590.1 GI:6012175
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SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (sites) Shimada,T., Kawai,T., Takeda,K., Matsumoto,M., Inoue,T., Tatsumi,Y., Kanamaru,A. and Akira,S.
IKK-1, a novel lipopolysaccharide-inducible kinase that is related to IkappaB kinases
Int. Immunol. 11 (8), 1357-1362 (1999)
JOURNAL MEDLINE
99352266
2 (bases 1 to 2154)
REFERENCE
AUTHORS Akira,S. and Shimada,T.
TITLE Direct Submission
Submitted (29-JUL-1998) Shizuo Akira, Hyogo College of Medicine, Department of Biochemistry, Mukogawa-cho 1-1, Nishinomiya, Hyogo

663-8501, Japan (E-mail: akira@yo-med.ac.jp, Tel: 81-798-45-6357,
Fax: 81-798-46-3164)

FEATURES

source

Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 REFERENCE
 AUTHORS Peters, R.T., Liao, S.M. and Maniatis, T.
 TITLE IKKepsilon is part of a novel PMA-inducible IkappaB kinase complex
 JOURNAL Mol. Cell 5 (3), 513-522 (2000)
 MEDLINE 20337984
 JOURNAL 2 (bases 1 to 2151)
 AUTHORS Peters, R.T., Liao, S.M. and Maniatis, T.
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 BASE COUNT 480 a 612 c 667 g 392 t
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 Query Match 99.8%; Score 2149.4; DB 9; Length 2151;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 361 gccgcataaacacactgtgaggagaaacggcattgtcatctgcgaatcaaacggggagac 420
 Oy 423 atcatgacctctgtagggagagagggagagagatcatcaaaagtctgcaagcttcgagct 482
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 Oy 543 catcccgacatgatgagagggcggtgtctgaaagcccgagaaaaaggtctgggtg 602
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 Oy 663 ttcatcccttctgtgtgagcagcgagaaacagagatcatgtaccgatacacaagag 722
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 Oy 1383 gcaagagacatccctctctactcactcagcagcagcgtggaactgagaggtctcagcagcgtg 1442
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 Db 1897 TGAGAAAGATGCTTCATCTTACGAGAGAGCTG 1928

RESULT 7
 AF145705 2201 bp mRNA linear ROD 02-JUN-1999
 LOCUS Mus musculus r2k protein kinase homolog mRNA, complete cds.
 DEFINITION AF145705
 ACCESSION AF145705.1 GI:4960037
 VERSION
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 Mus musculus homolog to human r2k cDNA
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 2201)
 AUTHORS Wisniewski, D. and Marcy, A.I.
 REFERENCE Direct Submission
 TITLE Submitted (26-APR-1999) Molecular Design and Diversity, Merck and Company, 126 East Lincoln Avenue R50A-300, Rahway, NJ 07065, USA
 JOURNAL Location/Qualifiers
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 SOURCE 1..2201
 /organism="Mus musculus"
 /strain="Swiss-Webster/NIH"
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 /protein_id="A034590.1"
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 /translation="Most N-terminal residues are conserved with the human r2k protein kinase homolog."
 CDS
 BASE COUNT 663 a 469 c 560 g 509 t
 ORIGIN

Query Match 25.7% Score 553.6; DB 10; Length 2201;
 Best Local Similarity 57.1%; Pred. No. 1.2e-90;
 Matches 1081; Conservative 0; Mismatches 784; Indels 27; Gaps 3;

QY 1 agatgcagagacagacacattactgttgacacagatgacctgtgggagcaggggcca 60
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 QY 61 ctgcagtggtgtacagagcccgcaacagaaatcccgagagctggtgtgtgaaggtct 120
 Db 70 CTGCAGAAATGCTTCCTCCGAGGAGCATAGAAACTGCTGATCTCTATGCTGCAAGATAT 129
 QY 121 tcaactactacagctactctgcgcccgcgagtgacgtgagggaggttgaggtctgc 180

Db 130 TTAATAACATTAACCTTCCTCCGCCAGTGAATGTTCAATGAGAAATTTAAAGTTAA 189
 QY 181 ggaagctgaaccccccgaacatcgtcaagctcttgcgtgagagagcagcggagcc 240
 Db 190 AAAAATCAATCAACAAAACATTTGTAAGTTATTGCTTTTAAAGAGACAAACAA 249
 QY 241 ggcagaagctacgtgtgagtagtactgtcagtgagagcctgtgagtgctgtgaga 300
 Db 250 GACTTAAGTGTATTATGAGTATTGTCCTGAGTATGATACAGTATTCAGAGG 309
 QY 301 gccctgagaatgcccttggctgtcctgagagagagtgcttctgtgtgtgtgtg 360
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 QY 361 tggcgcagatgaacacacctcgtgagagagacatgtgtgacatcgacacagccgggga 420
 Db 370 TGGCGGAGATGATATCTCCGAGAGACGCGCATATGACCGAGATATCAAGCCAGCA 429
 QY 421 acatcatgcgctcgttagggagagagagagacatctacaagctgacagacttcgcg 480
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 QY 481 ctgcgcggagctgtgagtagatgagagagagtgctcgtgtgtgtgtgtgtgtgtgt 540
 Db 490 CCGCTCGAGACTGAGAGACGATAGCATGTTGTGTCTGTGAGGCGACAGAAAGATAC 549
 QY 541 tgcacccagacatgtatgagcggcggcgtgtctgcgaagcccccgaacaaacgcttggg 600
 Db 550 TGCAATCCGAGCATGATGAAAGGCGCATGTAAGAAAGGCGCATGAGAAATACGAGG 609
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 Db 730 GGAAGCGCTGTGCTGCAATATCTGAGATGAGAAAGGAGAAAGGAGCAATATGACTGA 789
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Db 661 CAACAGTATTTGGAGCATGGGATACATTTTACCATGACACTCTGATGATCAGC 720
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 Qy 721 aagaacggctggagcattgaggtgcccagagcgaggaacggccccggaggtgga 780
 Db 781 GAAAGCTTCTGTCATATCTGAGATACAGAAAGCAGAAATGACCAATGCTGGA 840
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 Qy 961 tccctgacacatctatactcctgacagcagacacagatagcatttccagagcgctgac 1020
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RESULT 9
 ARO16417 2994 bp DNA linear PAT 05-DEC-1998
 LOCUS ARO16417
 DEFINITION Sequence 1 from patent US 5776717.
 ACCESSION ARO16417
 VERSION ARO16417.1 GI:3972694
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2994)
 AUTHORS Cao, Z.
 TITLE I. kappa. B kinases
 JOURNAL Patent: US 5776717-A 1 07-JUL-1998;
 FEATURES
 source 1..2994
 location/Qualifiers
 BASE COUNT 1018 a 489 c 611 g 876 t
 ORIGIN

Query Match 21.5%; Score 463.4; DB 6; Length 2994;
 Best Local Similarity 59.0%; Pred. No. 2, 6e-74;
 Matches 794; Conservative 0; Mismatches 551; Indels 0; Gaps 0;

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 Db 131 CTGGCAATGTTCTTCGTGGAAGACATTAAGAACTGGTGATTTATTTGCTATATAAGTAT 190
 Qy 121 tcaacactaccagctacatcgcgcccccgaggtgacagtgaggaaggtttgaagctctgc 180
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 Qy 181 ggaagctgaaccacacagacatcgtcaagctcttgcggtgagggagagcgagcggaagcc 240
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 Db 551 CAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTT 610
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 Db 611 TGCACCTGATATGATATGAG 670
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LOCUS	AF174536	2190 bp mRNA linear PRI 10-MAY-2000
DEFINITION	Homo sapiens NF-kB-activating kinase NAK mRNA, complete cds.	
ACCESSION	AF174536	
VERSION	AF174536.1	GI:7767392
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 2190)	
AUTHORS	Tojima,Y., Fujimoto,A., Delhase,M., Chen,Y., Hatakeyama,S., Nakayama,K., Kaneo,Y., Nimura,Y., Motoyama,N., Ikeda,K., Karin,M., and Nakanishi,M.	
TITLE	NAK is an Ikkappa kinase-activating kinase	
JOURNAL	Nature 404 (6779), 778-782 (2000)	
MEDLINE	20244479	
PUBMED	10783893	
REFERENCE	2 (bases 1 to 2190)	
AUTHORS	Tojima,Y., Fujimoto,A., Hatakeyama,S., Nakayama,K., Kaneo,Y., Nimura,Y., Motoyama,N., Ikeda,K., Karin,M., and Nakanishi,M.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-AUG-1999) Biochemistry, Nagoya City University Medical School, Kawasumi I, Mizuno-ku, Mizuho-cho, Nagoya, Aichi 467-8601, Japan	
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BASE COUNT	757 a	360 c 460 g 613 t
ORIGIN		
Query Match	21.4%; Score 461.4; DB 9; Length 2190;	

Best Local Similarity 59.08; Pred. No. 6,3e-74;
Matches 792; Conservative 0; Mismatches 551; Indels 0; Gaps 0;

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423 atcagagcctcgttagaggagagggagagacatctcaagctcagagctcggcgct 482
421 ATCATGCGCTGTATAGCGGAAGATGAGAGTGTGTCTGTAACAACTCAGAGATTTGGTGCA 480
483 gccggagagctgagatgagatgagaagtlcgtcgtcgtctatggagctgagggagtaactg 542
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RESULT 14
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LOCUS AF197914 melanogaster protein kinase Dlk2 (dlk2) mRNA, complete
DEFINITION cds.
ACCESSION AF197914
VERSION AF197914.1 GI:6166486
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Diptera; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscophora; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 2136)
AUTHORS Inohara, N.
TITLE Dlk2, 1K-1 like protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2136)
AUTHORS Inohara, N.
TITLE Direct Submission
JOURNAL Submitted (22-OCT-1999) Department of Pathology, Comprehensive
Center, University of Michigan Medical Center, 1500 E.
Medical Center Dr., Ann Arbor, MI 48109, USA

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2002, 08:32:07 ; Search time 725.44 Seconds
(without alignments)
5097.918 Million cell updates/sec

Title: US-09-582-397A-1

Perfect score: 2154
Sequence: 1 agatgcagagcacagccaat.....agcactcctgagtctgag 2154

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2154	100.0	2154	21	AAA52448 Human I-kappa-B k1
2	2152.4	99.9	3221	21	AAA47001 DNA encoding a hum
3	1506.2	69.9	2910	21	AAA52449 Murine I-kappa-B k
4	1506.2	69.9	3385	21	AAZ5275 Murine I-kappa B k
5	553.6	25.7	3219	21	AAZ5276 Murine I kappa B k
6	463.4	21.5	2994	19	AAV36086 cDNA encoding a hu
7	463.4	21.5	2994	20	Human TRAF2-associ
8	463.4	21.5	3013	22	AAFA4626 Novel protein kina
9	463.4	21.5	3372	22	AAAI4494 Human inhibitory k

10	461.8	21.4	3034	21	AA292224 Human cell signal
11	375.6	17.4	2187	23	ABL04897 Drosophila melanog
12	365.6	17.0	511	22	AA527175 cDNA encoding nove
13	358	16.6	4518	23	ABU04896 Drosophila melanog
14	227	10.5	3511	23	ABLI6432 Drosophila melanog
15	178.2	8.3	538	22	AA527160 cDNA encoding nove
16	170	7.9	949	22	AAH95884 Human protein enco
17	166.8	7.7	3641	21	AAZ58582 Mouse protein kina
18	144	6.7	2371	21	AAZ58583 Mouse protein kina
19	91.6	4.3	198	21	AAAI4461 Human secreted exp
20	91.6	4.3	339	20	AAAI1125 Human secreted pro
21	87.8	4.2	302	20	AAAI0308 Human secreted pro
22	87.8	4.1	2268	20	AAAI1590 Human inhibitor-ka
23	87.8	4.1	2268	20	AAH98271 cDNA encoding huma
24	87.8	4.1	2268	20	AAH99304 Human IKK-beta cod
25	87.8	4.1	2268	20	AAH84689 Human I-kappa B k1
26	87.8	4.1	2268	20	AAH84689 Human I-kappa B k1
27	87.8	4.1	2268	21	AAH84689 Human I-kappa B k1
28	87.8	4.1	2268	24	AAH96316 Human IKKbeta enco
29	87.8	4.1	2271	19	AAV22842 DNA encoding inhib
30	87.8	4.1	2291	19	AAV32970 Human I-kappa-B k1
31	87.8	4.1	2998	21	AAE21148 Human low adenosin
32	87.8	4.1	3018	21	AAAI4560 DNA encoding a GFP
33	87.8	4.1	3024	21	AAAI4558 DNA encoding a I-k
34	87.8	4.1	3058	21	AAAI5026 Human adenosine re
35	87.8	4.1	3965	20	AAH9675 Full length IK-Bet
36	87.8	4.1	8631	21	AAE21150 Human low adenosin
37	87.8	4.1	8631	21	AAAI5028 Human adenosine re
38	86.8	4.0	775	20	AAAI5875 cDNA encoding helli
39	74	3.4	1469	20	AAH9676 N-terminal Kinase
40	69	3.2	1795	22	AAE74523 Mouse Lkbl encodin
41	69	3.2	1795	22	AAE92270 Mouse Lkbl cDNA se
42	66.8	3.1	1302	17	AAH38285 Protein kinase cDN
43	66.8	3.1	1302	20	AAH79647 Human Lkbl coding
44	66.8	3.1	1302	20	AAH39660 Renal cancer assoc
45	66.8	3.1	1302	24	ABA03938 Human STK11 coding

ALIGNMENTS

RESULT	1
AAA52448	standard; cDNA; 2154 BP.
ID	AAA52448
XX	AAA52448;
AC	25-SEP-2000 (first entry)
DT	Human I-kappa-B kinase (IKK-1) cDNA.
DE	Human I-kappa-B kinase (IKK-1) cDNA.
XX	Human I-kappa-B kinase (IKK-1) cDNA.
KW	nuclear factor kappa-B; inflammation; immune disorder; TRAF molecule;
KW	I-TRAF related disorder; antiinflammatory; immunostimulatory; ss.
XX	Human sapiens.
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XX	Human sapiens.
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PN	WO200024908-A1.
XX	04-MAY-2000.
PD	04-MAY-2000.
XX	26-OCT-1999; 99WO-JP05916.
PE	26-OCT-1999; 99WO-JP05916.
XX	26-OCT-1998; 98JP-0304085.
PR	26-OCT-1998; 98JP-0304085.
XX	(NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA	(NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX	Akira S, Shimada T;
PI	Akira S, Shimada T;

[illegible]

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RESULT 4
AA295275
AA295275 standard; cDNA; 3385 BP.
AA295275:
26-MAY-2000 (first entry)
Murine I kappa B kinase-related kinase 1 encoding cDNA SEQ ID NO.1.
Mouse; murine; I kappa B kinase-related kinase; IKR-1; IKR-2;
protein kinase; immunomodulatory; antiinflammatory; antimicrobial;
cytostatic; autoimmune; inflammatory; infection; neoplastic disease; ss.
Mus sp.
Location/Qualifiers
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17-FEB-2000.
04-AUG-1999; 99MO-US17578.
04-AUG-1998; 98US-0095269.
11-SEP-1998; 98US-0099973.
05-FEB-1999; 99US-0118783.
(IMMUNEX CORP.
Bird TA, Valra GD;
WPI: 2000-195583/17.
P-PSDB; AAY80279.
Novel kappa B-kinase related kinases IKR-1 and IKR-2 used as molecular weight markers and in peptide fragmentation studies -
Claim 1; Fig 1; 85pp; English.
The present sequence encodes murine I kappa B-kinase related kinase 1 (IKR-1). IKR proteins have immunomodulatory, antiinflammatory, antimicrobial and cytostatic activities. IKR polynucleotides can be used to express the proteins, and as probes to identify nucleic acids encoding proteins having kinase activity. IKR-1 and IKR-2 proteins and fragmented polypeptides are used for purifying proteins, e.g. to purify binding partner proteins; to measure protein activity, e.g. as quality assurance agents to monitor shelf life and stability of binding partner proteins. They may also be used as research agents, e.g. in assays to determine protein kinase activity, to identify novel molecules involved in signal transduction pathways, and to identify therapeutic compounds, to identify substances which interfere with the rate of substrate phosphorylation (such compounds would be useful for the treatment of autoimmune, inflammatory, infectious or neoplastic diseases), as molecular weight and isoelectric focusing markers, as controls for peptide fragmentation, identification of unknown proteins, e.g. by comparison with proteins in databases and for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunofluorescence chromatography. The antibodies can also be used to block binding of the IKR polypeptides to their binding partners.
Sequence 3385 BP; 821 A; 922 C; 925 G; 717 T; 0 other;

Query Match 69.9%; Score 1506.2; DB 21; Length 3385;
Best Local Similarity 82.1%; Pred. No. 0;

Matches 1775; Conservative 0; Mismatches 373; Indels 15; Gaps 3;
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Oy	1315	taatgtctcggggggtctgcaactgtgtaatactgaaagtgcgtcccaagggcccaatgcaagcagctc	1374
Db	1688	tgatgtctcgggggtctaatcttgggtcccttggaaggtgtctcagagacacgtgcgaagcaaac	1747
Oy	1375	tgaagctgcgaaggaacatccctctcttaacctcaagcagcagctcgtggaactgagagttca	1434
Db	1748	tgagagctcaacacagcagccctctcttaacctcaagcagcagctcgtggaactgaaagttca	1807
Oy	1435	gcaacgcgtgcctgcgaacccctgcgaatacccaaggaactggaaggcggtctgcbaaacctgaggtcca	1494
Db	1808	gcaactggaagcggggagatgcctgcgaatcccaaggaaggaaggaaggtccacagagcttaagaaacca	1867
Oy	1495	ggctcggcagactctagcgggaagctccctctccagaatgctccccaataatctccgggaagaccagg	1554
Db	1868	ggctcggcagactctctcagagatccctctgtcttaaatgtctccacaatgtctcagaaaacccaa	1927
Oy	1555	aggaacctgcgaagcagctgcgaacggggagctcgtgtgaaggccgggaatcaaggtatactgag---	1611
Db	1928	ggaacctgcgaagctcgtctcgggttgaaagaccttcttaaggaacccgggaaccagatctcaatggagata	1987
Oy	1612	acgaacaacatcccaacaaattcaatgctcgttttggaacaagaatgaactctcaacaacagt	1671
Db	1988	acaaagatccccaagaaattccagttgctgttttggaacaagaatgcaactctcaacaacagt	2047
Oy	1672	tcaagaagctctahgatatgaggccaagggctcgtgctacacaaggaagagagatctcaacaagctcgg	1731
Db	2048	tcaagaatactcaagatatgaggccaagggctcgaagctacaaatgaggaagatctcaacaagctcgg	2107
Oy	1732	ataagctggaattctaatgcatcttttgccaagaagactcctcgtgaaggtgtctcaggagaggtctcg	1791
Db	2108	ataaggtataaattctaatgcatctcttgccaagaaggtcgtctgtaaggtgtctctcaggagaggtctcg	2167
Oy	1792	tgcgaagatatacaagcgctctcttgatcaacaacggccaaggaagggtgggtgtgtgcacgga	1851
Db	2168	tgcgaagctatcaaggtctcgtcgtgtcgaacaacggccaaggaagggtgggtgtgtgcacgga	2227
Oy	1852	ccaagaaaccaactgcgcctcgtgttggtgtctgtctgtggctcgtctgtataccaagaacggcccg	1911
Db	2228	ccaagaaaccaactgcatactatctatctgtgcgaactcgtgtggccaacctgtatactcggagccggg	2287
Oy	1912	gggtcccaaggaaggtcttaagaaagctcctcgtgaagaggtatctacaagctctctctcaagacc	1971
Db	2288	gagccccaaggaaggtcttgaanaaagatctctgtataagctctctcttgagacaagaggtctccgaac	2347
Oy	1972	gagcaaaagggggtctcagagcctctgcgcgcgtccccaatactctctacacccggcctctacaaga	2031
Db	2348	-----agggaagctggaaggtgtcaacgcgaacactatgctctctataccgcgcctgataccga	2401
Oy	2032	aggaactgtctctcacatgcaagagcctctgcaggaggatgaagctgtctgcatgaac	2091
Db	2402	aggaactgtctctcacatgcaagagcctctgtataatgatatgaagctatgtgcctctgtac	2461
Oy	2092	tcctcggcaaaaacacggaatactcgaacgggttaaatgatactccagcaactcctgttgtct	2151
Db	2462	tcacggataaaaacacggaactcatcgaaggttataatgagatctccatctcggaaccaagctgtct	2521

YY	2152	gag	2154	
		111		
Db	2522	gag	2524	
RESULT	5			
ID	AA295276			
XX	AA295276 standard; cDNA; 3219 BP.			
AC	AA295276;			
DI	26-MAY-2000 (first entry)			
XX				
DE	Murine I kappa B kinase-related kinase 2 encoding cDNA SEQ ID NO:3.			
XX				
KM	Mouse; murine; I kappa B kinase-related kinase; IKR-1; IKR-2;			
KW	protein kinase; immunomodulatory; antiinflammatory; antimicrobial;			
KX	cytostatic; autoimmune; inflammatory; infection; neoplastic disease; ss.			
OS				
Mus sp.				
XX				
Key	Location/Qualifiers			
EH	212..2401			
FT	CDS			
FT	/*tag= a			
FT	/product= "IKR-2"			
FT	/note= "I kappa B kinase-related kinase 2"			
XX				
PN	WO200008179-A1.			
PD	17-FEB-2000.			
XX				
PF	04-AUG-1999; 99WO-US17578.			
XX				
PR	04-AUG-1998; 98US-0095269.			
PR	11-SEP-1998; 98US-0099973.			
XX	05-FEB-1999; 99US-0118783.			
XX				
PA	(IMMV) IMMUNEX CORP.			
XX				
PI	Bird TA, Vitca GD;			
XX				
DR	WPI; 2000-195583/17.			
XX	P-ESDB; AAY80280.			
PT	Novel kappa B-kinase related kinases IKR-1 and IKR-2 used as molecular			
XX	weight markers and in peptide fragmentation studies			
PS	Claim 1; Fig 2; 85pp; English.			
XX				
XX				
CC	The present sequence encodes murine I kappa B-kinase related kinase 2			
CC	(IKR-2). IKR proteins have immunomodulatory, antiinflammatory,			
CC	antimicrobial and cytostatic activities. IKR polynucleotides can be			
CC	used to express the proteins, and as probes to identify nucleic acids			
CC	encoding proteins having kinase activity. IKR-1 and IKR-2 proteins and			
CC	fragmented polypeptides are used for purifying proteins, e.g. to purify			
CC	binding partner proteins; to measure protein activity, e.g. as quality			
CC	assurance agents to monitor shelf life and stability of binding partner			
CC	proteins. They may also be used as research agents, e.g. in assays to			
CC	determine protein kinase activity, to identify novel molecules involved			
CC	in signal transduction pathways, and to identify therapeutic compounds,			
CC	to identify substances which interfere with the rate of substrate			
CC	phosphorylation (such compounds would be useful for the treatment of			
CC	autoimmune, inflammatory, infectious or neoplastic diseases), as			
CC	molecular weight and isoelectric focusing markers, as controls for			
CC	peptide fragmentation, identification of unknown proteins, e.g. by			
CC	comparison with proteins in databases and for preparation of antibodies			
CC	The antibodies can be used in assays to detect the presence of the			
CC	protein, and to purify the protein by immunoaffinity chromatography. The			
CC	antibodies can also be used to block binding of the IKR polypeptides to			
XX	their binding partners.			
XX				
Sequence	3219 BP; 933 A; 672 C; 791 G; 823 T; 0 other;			

Query Match 25.7%; Score 553.6; DB 21; Length 3219;
 Best Local Similarity 57.1%; Pred. No. 6e-117;
 Matches 1081; Conservative 0; Mismatches 784; Indels 27; Gaps 3;

QY 1 agatgcagagacaccccaattactctgtgcacacagatgacctgcgtggcgaggcgca 60
 Db 210 agatgcagagacaccccaattactctgtgcacacagatgacctgcgtggcgaggcgca 269
 QY 61 ctgcacgtgtgtacaagggcccgacacagaatcccgagagctgtgtgtgtgtgtgtgt 120
 Db 270 ctgcacgt 329
 QY 121 tcaaacctacacagctacacgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgt 180
 Db 330 ttaataacataagcttcttcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgt 389
 QY 181 ggaagctgaac 240
 Db 390 aaaaactcaatcaaaaaaactcaatcaatcaatcaatcaatcaatcaatcaatcaat 449
 QY 241 ggcagaagctacgt 300
 Db 450 gacataaagctatattatattatattatattatattatattatattatattatattat 509
 QY 301 gccctggaagtgccttgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgt 360
 Db 510 agcgtccaatgtcgt 569
 QY 361 tggccgcagac 420
 Db 570 tggccgcagac 629
 QY 421 acatcatgcgcctcgt 480
 Db 630 acatcatgcgcctcgt 689
 QY 481 ctgc 540
 Db 690 cgcctcgc 749
 QY 541 tgcacccgcacatgtatgc 600
 Db 750 tgcacccgcacatgtatgc 809
 QY 601 tgcactgt 660
 Db 810 ctacgcgt 869
 QY 661 ccttcaccccttgcgt 720
 Db 870 cgittagaccccttgcgt 929
 QY 721 agaaagccgcgt 780
 Db 930 ggaagccgcgt 989
 QY 781 gctacacccctcctac 840
 Db 990 gtggagacatgcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1049
 QY 841 tctgtgcac 900
 Db 1050 tctgtgcac 1109
 QY 901 cggagac 960
 Db 1110 cagagac 1169
 QY 961 tctgtgcac 1020
 Db 1170 cggagac 1229

QY 1021 acaagcagac 1080
 Db 1230 ataaac 1289
 QY 1081 tctcgaagccac 1140
 Db 1290 tctcgaagccac 1349
 QY 1141 ccccttcgac 1200
 Db 1350 tgc 1409
 QY 1201 ccaagcttcctcccaaaagtggaac 1260
 Db 1410 ctaaaataac 1469
 QY 1261 ggc 1320
 Db 1470 ggc 1529
 QY 1321 ttcgc 1375
 Db 1530 gaaaggggttgc 1589
 QY 1376 -----ggaagtggaagac 1428
 Db 1590 agaaagcagaggt 1649
 QY 1429 ggttc-----agcagcgt 1482
 Db 1650 aagtgatgt 1709
 QY 1483 aactgt 1542
 Db 1710 acataac 1769
 QY 1543 cggagac 1602
 Db 1770 aggac 1829
 QY 1603 ta-----catgt 1653
 Db 1830 aagtcac 1889
 QY 1654 actcatcacaac 1713
 Db 1890 cggagac 1949
 QY 1714 agcagattcacaac 1773
 Db 1950 aacagatcacaac 2009
 QY 1774 ttttcagagagagtggt 1833
 Db 2010 acttcacagagagtggt 2069
 QY 1834 tgaagtggt 1865
 Db 2070 tgaagtggt 2101

RESULT 6
 AAV36086
 ID AAV36086 standard; cDNA: 2994 BP.
 XX
 AC AAV36086;
 XX
 DT 02-SEP-1998 (first entry)
 XX
 DE cDNA encoding a human TK2 protein.
 XX
 KW Human; TK2 protein; TK2-specific activity; phosphorylation; Ikappab; IKb; screening; IKb serine 36-specific kinase; TK2-specific binding agent;

RESULT 7
 AAV62697 standard; cDNA; 2994 BP.
 AC AAV62697;
 XX 21-JAN-1999 (first entry)
 DE Human TRAF2-associated kinase (TK2) encoding cDNA.
 XX
 KW TK2 protein; immunogen; transcriptional regulator; screening; human;
 KW gene therapy; diagnosis; IkappaB kinase; NF-kappaB transcription factor;
 KW drug development; TRAF2-associated kinase; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 73..2262
 FT /tag= a
 FT /product= "TK2 protein"
 XX
 XX US5837514-A.
 XX
 PD 17-NOV-1998.
 XX
 PF 07-MAR-1997; 97US-0812533.
 XX
 PR 07-MAR-1997; 97US-0812533.
 XX
 PA (TULIA-) TULARIK INC.
 XX
 PI Cao Z;
 XX
 DR WPI: 1999-023452/02.
 DR P-SDB; AAW79273.
 XX
 PT Recombinant or isolated nucleic acid encoding TRAF2-associated
 PT kinase - which regulates inhibitors of NF-kappaB transcription
 PT factors, useful as immunogen; for isolation of other transcriptional
 PT regulators; in drug screening; and in gene therapy
 XX
 PS Claim 4; Columns 9-16; 11pp; English.
 XX
 CC This cDNA encodes a TK2 (TRAF2-associated kinase) protein belonging to
 CC the family of IkappaB kinases. Cells containing a recombinant TK2 nucleic
 CC acid are used to produce the TK2 protein which is useful as immunogen,
 CC for isolation of other transcriptional regulators and in drug screening.
 CC The TK2 nucleic acid and corresponding antisense sequences, are useful
 CC in gene therapy to modulate TK2 expression, and its fragments are used as
 CC probes and primers in diagnostic assays (hybridisation or amplification),
 CC for identification of related sequences and to detect wild-type or mutant
 CC alleles. The TK2 nucleic acid can also be used to create transgenic
 CC animals for studying the efficacy of candidate drugs. TK2 binding agents
 CC are useful in diagnosis, therapy and drug development, e.g. they can
 CC activate, inhibit or alter TK2-dependent processes and activity of NF-
 CC kappaB transcription factor.
 CC
 SQ Sequence 2994 BP; 1018 A; 489 C; 611 G; 876 T; 0 other;

Query Match 21.5%; Score 463.4; DB 20; Length 2994;
 Best Local Similarity 59.0%; Pred. No. 2,6e-96;
 Matches 794; Conservative 0; Mismatches 551; Indels 0; Gaps 0;

QY 1 aggtgcagagcagcaatctacgttgacacagatgacctgcgggacagggccca 60
 DB 71 agatgcagagcacttcaacatcctggtcttattctgatatattagcgaagagccta 130
 QY 61 ctgcacagtgtacaagcccgcaacaagaatccgagagctggttgcgtgaaggtct 120
 DB 131 ctgcgaatgtcttctggtgaagacataagaactggtgattatttgcatacaaggtat 190
 QY 121 tcaaacactaccagctactcgtgcgcccgcgagtgtagagtgaggttgaggtctctgc 180

DB 191 ttaataacataagcttcctcgtccagtgatgtccaatagtgagagatttgaagtggtga 250
 QY 181 ggaagctgaacacacagaaacatcgtcaagctcttgcgttgagagagcggcggaagcc 240
 DB 251 aaaaactcaatcaaaaataatgtccaataattatgtctattgaagagagacaacaa 310
 QY 241 ggcagaagtgactggtgatgagtgactgtccaggtggagagcctgtgtgtgtgcga 300
 DB 311 gacataaagtactattatagaaatttgcacatgagagaggttatacactgttttagaag 370
 QY 301 ggcctgagaatgccttgcgtgcgctgagagatgaatcctgtgtgtgtgtgtgtgtg 360
 DB 371 aaccttcaatgcctatgagactacacgaactcgaatctcgaattcttctgtgtgtgtgt 430
 QY 361 tggcgcgtatgaacacactcgcgggagagacgcatgtgcatcgcagatcaagccgggga 420
 DB 431 tgggtggaatgatcatctacagagagaaatggtatagtgacacgtgatatacgaagcagga 490
 QY 421 acatcagtcgctcgtgagggagggagagagagagagagagagagagagagagagagag 480
 DB 491 atatcgtcgtgttataagggagagatgagacagtcctgttacaactcacaatatttggtg 550
 QY 481 ctgcccggagagctgatagtatgaatgagagctcgtcgtctatgtgagactgagatacc 540
 DB 551 cagctagagaattagaagatgtatgagcaggttcttctcgtgtatgacagagaataatt 610
 QY 541 tgcattccgacatgatatagcgcggtgctcgtcgaagcccgcaaaaagcgttcgggg 600
 DB 611 tgaacccgtatagtatgagagagacagtgcttaagaagaatatacagaagaataatgag 670
 QY 601 tgaactgatatctcgtgaacatctgagtgactgtacatgacatgacagcactgacgctgc 660
 DB 671 caaagcttgatctcttggagcatttgggtgaacatttacaatgcagctctgtatcaccgc 730
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 DB 731 catltagaccccttgaagggcctcgtlagaataaagagtggtatataaataatatacag 790
 QY 721 agaagcggcgtggtggcattgtcagatgtcccaagagcgagagagagcgccttgagatga 780
 DB 791 gaagccttcgtgtgcaaatatctgtagatgaagaagcaaatatgacaatttgactga 850
 QY 781 gctacacccctcccatcactcagctgcagctgtacatgaggtgagcgagcgtgtggcca 840
 DB 851 gggagagactcgtcttcttctgacgtcttctccggggtcttcaggttacttaccctg 910
 QY 841 tccctgcaacaatcctgtgaggtgagcgagcgagagctgtggtcgtcagcaagttcttg 900
 DB 911 tcttgcacaacatccttgaagagatcagagaaagtgttggtgtttgacagatttttg 970
 QY 901 cggagacccgtgtacatccctgcagcgaggtgtgtccatgtcttccctgtccagagag 960
 DB 971 cagaaactagtgatatacttccacgaaatcgttaattcattgttcttcgtatacaaaatga 1030
 QY 961 tccctgacacatctatactcatgtcccaacaacagatagccatttccagagagcggtgc 1020
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 QY 1021 acaagcagacagtggtgcccccgacacacagaggtactccttggaggttcaactctgtg 1080
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 QY 1141 ccccttgaagcagacatcccttaaggggtcgtcctttagggagccctgtctgtgagctcc 1200
 DB 1211 ttgtgtgaagccgggaacctctgaataccatagaggtatataatgaaaaaatctccctcc 1270
 QY 1201 ccaagctgtccccaagatgagcctgcagcgaggtatcaaaactgtccaaagggcgtgtgtg 1260


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Db 1059 gtggagacatgctcttcttctgacgtcttctcgggggcttcaagttcttaccctcg 1118
QY 841 tcttggccaaacatccttggaagtgagccaaagtgtctggggtctcaccagttcttgg 900
Db 1119 tctctgcaacaacatccttggaagtgagccaaagtgtctggggtctcaccagttcttgg 1178
QY 901 cggagacagatgacatcctcgcagcagatgtctgcacatgtcttctcccttccagcag 960
Db 1179 cagaaactatgtatatacttctcgcgaatggtatctatgttttcttcacacaaatga 1238
QY 961 tcttcacacacatcatatccatgcgcacacacagatagccatttccagagagccgtgc 1020
Db 1239 cagctcacaagaattatatactatactataacgcgtactatattcactgaactgtgat 1298
QY 1021 acaagcagaacagatgttggccccccacacacagagtaaccttcttgaggtcactctgtg 1080
Db 1239 ataacaacaacaaattatttctcaaatcaagaactatctacgaagggagacgttag 1358
QY 1081 tcttcgaagccacagctctcagacagacacatgcgccacacagcagcagcagccctga 1140
Db 1359 tcttgaacacctggaagcgtcgcacacacatttccctaaacactatgaggaacccatata 1418
QY 1141 ccccttcagacacagccatccctlaaggggcttgccttcagggaccctgtctctgagcgtcc 1200
Db 1419 ttgtagtaagccgggaacctctgaataccatagatataatatagaaaaaatttccctcc 1478
QY 1201 ccaagttctgtcccaagatgagcctgcagcaggtattacaacatgccaaggcgtgtgtg 1260
Db 1479 ctaaaatcatcatcactatgatattagacgggagatgctagatgcttaagcacaataaag 1538
QY 1261 gcgcggcgtacacagcctcgtgagcagcagcgtcgtgagtgagtgaggaagagtaagt 1320
Db 1539 ggggtgtgtgtatgctgcgcagaaatgccagtaacctactgtcttatacgaatgaatgac 1598
QY 1321 ttcgggggctgactggtgcataga 1345
Db 1599 gaaaggagatacgtatgctgattga 1623

RESULT 10
AAZ29224
ID AAZ29224 standard; cDNA; 3034 BP.
AC AAZ29224:
XX
XX
XX 28-FEB-2000 (first entry)
DE Human cell signalling protein-3 encoding cDNA.
XX
XX Cell signalling protein-3; CSIRP-3; cell proliferation; arteriosclerosis;
XX inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;
XX Addison's disease; multiple sclerosis; ss.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 93.2282
XX FT /tag- a
XX FT /product- "Cell Signalling Protein-3"
XX
XX PN W0958558-A2.
XX
XX PD 18-NOV-1999.
XX
XX PF 13-MAY-1999; 99MO-US10567.
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XX PR 13-MAY-1998; 98US-0085343.
XX PR 26-AUG-1998; 98US-0098010.
XX
XX PA (INCY-) INCYTE PHARM INC.
XX
XX Bandman O, Hillman JL, Lai P, Yue H, Tang YT, Patterson C;

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PI Baughn MR, Yang J;
XX
XX WPI: 2000-086432/07.
DR P-PSDB; AAY44240.
XX
XX
XX Human cell signalling proteins useful for, e.g. diagnosing cell
XX proliferative and inflammatory disorders
XX
XX Claim 9; Page 81-82; 90pp; English.
XX
XX The present sequence is a cDNA obtained from Incyte clone 1250171 of
XX LUDGFET03 library. It encodes cell signalling protein-3 (CSIRP-3). It is
XX expressed in reproductive, haematopoietic/immune and nervous
XX tissues. Fragments of CSIRP encoding nucleic acid can be used as
XX hybridisation probe for detecting CSIRP related sequences or allelic
XX variants. Recombinant CSIRP can be produced in host cells by transforming
XX them with genetically engineered vectors. Agonists or antagonists can be
XX used in the treatment of cell proliferative and inflammatory disorders
XX associated with decreased or increased CSIRP expression. CSIRP is used in
XX the diagnosis, prevention and treatment of cell proliferative disorders
XX like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
XX disorders like AIDS, Addison's disease, multiple sclerosis, etc.
XX
XX Sequence 3034 BP; 1031 A; 496 C; 619 G; 888 T; 0 other;

Query Match 21.4%; Score 461.8; DB 21; Length 3034;
Best Local Similarity 59.0%; Pred. No 6,1e-96;
Matches 793; Conservative 0; Mismatches 552; Indels 0; Gaps 0;

QY 1 agatgcagagacagacccaattacctgtgcacacagatgacctgtggcaggggcca 60
Db 91 agatgcagagacacattcatcatctgtgcttattctgtatttgacgaaggagcta 150
QY 61 ctgcagtggtgtaaaagccgcgacaaagaattccggaagcgtgtgtgtgaagctc 120
Db 151 ctgcgaacgcttctcgtggaagacataaagaactgtgtatttcttcatcaagat 210
QY 121 tcaaacatcacagctacctgcgcgcgcgaggtgcaggtgaggaagttgaggtctgc 180
Db 211 ttaataacataagcttctcctcgtccatgtagtgcataagagaagaattggaagtgtga 270
QY 181 ggaagctgaaccacacagaacatcgtcaagctccttgcgtgaggaagacggcgagcc 240
Db 271 aaaaactcaatcacaaaataattgtccaattattgtcattggaagagagacaacaacaa 330
QY 241 ggcagaagtgactgtgtatgagtagctgcacagttgggaagcgtgtgtgtgtgaga 300
Db 331 gacataaagtaactatataatgaaatttgcacatgtgggaattatatacactgtttagaag 390
QY 301 gscctgagaatgcttggctgctcctgagagatgagttccgtgtgtgtgtgtgtgtg 360
Db 391 aaccttcaatgtcctatgagctacacgaatcgtgaattcctaattgttttgcagatgtg 450
QY 361 tggcggcatgaacacacctgcgggagaagcgaattgtcatcgacatcaaacgggga 420
Db 451 tgggtggaatgacatctacgagagaatgtatagtcgacgctgatatcaacgagaa 510
QY 421 acataatgcgctcgtgagggagggagggagacatctacaacgctgcgaacttcggcg 480
Db 511 atatcatgctgttataagggagaagatggagacgtgtgtacaacacacagatlttgggtg 570
QY 481 ctgcgggagcgtggaatgagatgagaagatgtctcctcgtgtctatggagctggaagtaac 540
Db 571 cagctagagattagagaagatgagcaggtgttcttctctgtatggcacagaagaatatt 630
QY 541 tgcattccgacatgatatgagcggcggtgtcttcgaagccccaagcaaaaagcgttcgggg 600
Db 631 tgcacctgatatgatatgagagcagctgtcaagaagaatcatccagaagaatatggag 690
QY 601 tgcattgatactctgagacatgagtgagacattgacacatgacacatgacgtgcacgtgc 660
Db 691 caacagttatcttggagcatctggggttaacatttaccatgcagactatggaacactgtgc 750

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OY	661	ccctccctccctttgttggccacggcggaacaaagagatcatgttaccggtatccaccacag	720
OY	661		720
Db	751	catcttagaccctcttgaagggtcccttgaaggataaaagaagtgatgtataaaataattcacg	810
OY	721	agaagccggtctggggccatttgcaggtgtcccgagaagcgagaaacgggccccttgagtgtga	780
OY	721		780
Db	811	gaaagcctctctgtgcaatattcttgagtacagaagaagcagaataatggaccattgacttcga	870
OY	781	gtctaacacctcccatcaccttgcagctgtgtcatcttgggtctgcagagccagttgtgtccga	840
OY	781		840
Db	871	gttggagacatgcgtttcttcttgcagcttcttctcgggtgtcttccaaagttctatcccttg	930
OY	841	tcctgtgccaacatccctggaggtgtggagccaagtgtgtctgggtcttcgacagttcttg	900
OY	841		900
Db	931	ttctctgaaacatccctcttgaaagcagatctcaggaanaagtgttgggttttggaccagtttttg	990
OY	901	cggagagccagtgacatcttcgcagcgagatgtgtctgtccatgttcttccctgtccagcgacg	960
OY	901		960
Db	991	caggaacatagtgtatctacttccaccggaatgttaattcactgttttctgcgtacaaacatga	1050
OY	961	tcctgtgccccatcttatccatgtgcccaacagatagccatttccaggaagcgctgc	1020
Db	1051	cagctctaagatttatatacataagttataatctgtactataatltcatgaactgtat	1110
OY	1021	acaagcagagccagtggtggccccccgcagacacagagagtlacctcttltgaaggttacctgtg	1080
OY	1021		1080
Db	1111	ataaacacaacaaatattatttcttcaaatccaagaactatctcaggaaggtgcagcttag	1170
OY	1081	tcctgtgagcccgatctctcagcaagcacatctgcacacagcgagcgacgccccttga	1140
OY	1081		1140
Db	1171	tcttagaaccttgaagaggtctgcacacaatcttcccttaaaactcttgagaaacccctatat	1230
OY	1141	cccccttcagcaacgcatctccctaaagggtgtgctgtcccttcagggagaccctgtctgtgacgtc	1200
Db	1231	ttgtagtgaagcgcggaacctctgtgaatacacataggatataatgaaaaaattcccttc	1290
OY	1201	ccaagcttgcgtccccaaggttgaccttgcagcgagatltacacacatgcgaaggcgltgttg	1260
OY	1201		1260
Db	1291	ctaaagtacatctcacgtgtatgtatttagacggtgagtctgacgtgtcgaagcgaataacag	1350
OY	1261	gcgcgcgctacacagggccctctgcgtctgtgcacggtgcccctgtgtgtatgtggcagagactaatgt	1320
OY	1261		1320
Db	1351	gggttgtgtgttgaatgccttgcagaatctgcagatlaaccttactgtcttatcatgaatattatgc	1410
OY	1321	ttcgggggtgcagctgggtcatgtga	1345
OY	1321		1345
Db	1411	gaaagggtgatacgaatggtctgatttga	1435
RESULT	11		
ABL04897			
ID	ABL04897	standard; cDNA; 2187 BP.	
XX	ABL04897:		
AC			
XX			
DT	26-MAR-2002	(first entry)	
XX			
DE		Drosophila melanogaster expressed polynucleotide SPO ID NO 9173.	
XX			
KW		Drosophila: developmental biology; cell signalling; insecticide;	
KW		pharmaceutical; gene; ss.	
XX			
OS		Drosophila melanogaster.	
XX			
PN	WO200171042-A2.		
XX			
PD	27-SEP-2001.		
XX			
PF	23-MAR-2001; 2001WO-US09231.		
XX			
PR	23-MAR-2000; 2000US-191637P.		
PR	11-JUL-2000; 2000US-0614150.		

XX (PEKE) PE CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EM;
PI
XX WPI: 2001-656860/75.
DR
XX P-PSDB: ABB60794.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
XX Claim 1; SEQ ID NO 9173; 21pp + Sequence Listing; English.
XX
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AB557737-AB672072).
CC
XX The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX Sequence 2187 BP; 613 A; 510 C; 582 G; 482 T; 0 other;

Query Match	Similarity	17.4%;	Score 375.6;	DB 23;	Length 2187;
Best Local	Similarity	60.8%;	Pred. No. 3e-76;		
Matches	631;	Conservative	0;	Mismatches 404;	Indels 3; Gaps 1;
QY	4	tgcagagcacagcccaattactctgtgcaacagatgacctgtctgggcagaggccactg	63		
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QY	64	ccaagtggttacaagcccgcaacaaagaatccggagagctgtgtcttgaaggtcttca	123		
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QY	124	acaactacacagctaccctgcggcccgacggatgttcaagtttagggagttttagtgcctgcga	183		
Db	182	atccctacagtcacatgtagccagccgctgtatgtgcagatgsgggagttctcgagccctcgaaa	241		
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Db	242	aggtaacacacagagataatagtaaaagctgtgttcgacatcgagagagatcaagsggggcggt	301		
QY	244	agaaggtactgtgtgatgagatctcgtccagctggagagccctgtcttgagttgtcgtcgagagcc	303		
Db	302	gtaaggtactgtgtgatgagagctctgcacagsgggagagttctttaacatccctggagcagtc	361		
QY	304	ctggaagatgccttgggcctgcgtcgaagatgagttccctggtgtgtgcgtgtgtgtgtgtgtg	363		
Db	362	ctgagagactctgtaagctctgcgcgggaacacagattcctgtgtgtcttvgaacactgtgtgcg	421		
QY	364	ccggctctgagacacactgcggggaggaagagatgtgtgatctgcagacatcaagccggsggaaca	423		
Db	422	cgggaatgtgaagacctgtgcgggataaacaagctgtgtgatctgcagatccgaaacccggaaaca	481		
QY	424	tcatgagctcttgaggggagggagggcagaagcatctacaaagcttgacagactccgcgcgtc	483		
Db	482	taatgaagttcatctccggsgagacgggcaaacacatacaagcttactgtttccggtgcgtc	541		
QY	484	cccggagagctgatatgatatgagaaagttcgtctcggltctatagggacttgagagttactctgc	543		
Db	542	ctagagaactgtggagataatcacgccgttctgcctctctatatacgcaacaagaagattacttc	601		
QY	544	atccgcgactgttatgtgsgcggtgcgtgtccctcgaaagaagcccaagaagaaggtctgggtgtga	603		
Db	602	atccgcgactctctacgagcgcgctctgtgtgtgaggaagcaaatccagcgatcgtgttcaaccgcca	661		

QY 604 ctgtgatctcttgagcatttgagatgaccttgcacatgacgacactgagccgtccct 663
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QY 664 tcatccccccttgggtggccagcgagcaagaagatcatctacgtatcacaagaga 723
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Db 1079 tgcacaacagagtgccgc 1096

RESULT 12

ID AAS27175 standard; cDNA; 511 BP.

XX AAS27175;

DT 07-NOV-2001 (first entry)

DE cDNA encoding novel signal transduction pathway protein, Seq ID 210.

XX Neuroprotective; cytosolic; dermatological; immunosuppressive; tumour;
XX antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
XX immune system disorder; rheumatoid arthritis; inflammatory condition;
XX organ transplant rejection; infection; hepatitis C; blood disorder;
XX sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
XX cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
XX reproductive system; gastrointestinal; liver disorder; AIDS; ss;
XX acquired immune deficiency syndrome.

OS Homo sapiens.

XX WO200154733-A1.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01312.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216680.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
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PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
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PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
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PR 22-AUG-2000; 2000US-0226686.
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PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
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PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0231969.
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PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0235837.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.

PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
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 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
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 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
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 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 XX
 PI
 XX
 XX WPI: 2001-465460/50.
 DR P-PSDB: AAU17258.
 DR
 XX
 XX Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders -
 XX
 PS Claim 1; SEQ ID No 210; 880pp; English.
 XX
 XX The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and

CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
 CC abnormalities (Down syndrome), ischemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC as stimulators of B-cell responsiveness to pathogens, activators of
 CC T-cells, to induce higher affinity antibodies, and as a means to induce
 CC tumour proliferation in pathologies e.g. acquired immune deficiency
 CC syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction
 CC pathway protein coding sequences and PCR primers of the invention.
 XX
 Query Match 17.0%; Score 365.6; DB 22; Length 511;
 Best Local Similarity 99.7%; Pred. No. 3; E-74;
 Matches 365; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 agatgcagagcagcagcattaccctgtggcacacagatgacgtctgtggcaggggcca 60
 Db 107 agatgcagagcagcagcattaccctgtggcacacagatgacgtctgtggcaggggcca 166
 QY 61 ctgccagtggttacaaagcccgcaacaagaatccggaagctgtgtgtgaagttct 120
 Db 167 ctgccagtggttacaaagcccgcaacaagaatccggaagctgtgtgtgaagttct 226
 QY 121 tcaactactacagctactctgtggcccgagtgagcagtgtaggaggtttgagttctgc 180
 Db 227 tcaactactacagctactctgtggcccgagtgagcagtgtaggaggtttgagttctgc 286
 QY 181 ggaagctgaaccacagacatgcgaagctcttgcgtgtgaagagcggcggaagcc 240
 Db 287 ggaagctgaaccacagacatgcgaagctcttgcgtgtgaagagcggcggaagcc 346
 QY 241 ggcctgagagatgcttggcgtgagtgagtgagtgagtgagtgagtgagtgagtgag 300
 Db 347 ggcctgagagatgcttggcgtgagtgagtgagtgagtgagtgagtgagtgagtgag 406
 QY 301 ggcctgagagatgcttggcgtgagtgagtgagtgagtgagtgagtgagtgagtgag 360
 Db 407 ggcctgagagatgcttggcgtgagtgagtgagtgagtgagtgagtgagtgagtgag 466
 QY 361 tggcgcg 366
 Db 467 tggcgcg 472
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 ABL04896
 ID ABL04896 standard; CDNA; 4518 BP.
 XX
 AC ABL04896;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 9170.
 DE
 XX
 XX Drosophila: developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 XX 27-SEP-2001.
 PD
 XX
 XX 23-MAR-2001; 2001WO-US09231.
 XX
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 XX P-PSDB; ABB60793.
 DR New Isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 XX interactions -
 PS Claim 1; SEQ ID NO 9170; 21pp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB101840-AB16175).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 4518 BP; 1219 A; 968 C; 1116 G; 1215 T; 0 other:

Query Match 16.6%; Score 358; DB 23; Length 4518;
 Best Local Similarity 61.2%; Pred. NO. 4e-72;
 Matches 596; Conservative 0; Mismatches 375; Indels 3; Gaps 1;

QY 68 tggatcaagggccgcaagaatccggagagctgtgtgtggaaggtcctaacc 127
 DB 1198 tggatcaaggggggtcaacaagaatccggagagctgtgtgtggaaggtcctaacc 1257
 QY 128 taccagtaacctgagcccgagagtgaggtgaggtgaggtgaggtgaggtgaggt 187
 DB 1258 ctacagtcacatgacgagcgaggtgaggtgaggtgaggtgaggtgaggtgaggt 1317
 QY 188 gaaccacagagatcagtaagctcttgcgtgaggtgaggtgaggtgaggtgaggtgaggt 247
 DB 1318 caaccacagagatcagtaagctcttgcgtgaggtgaggtgaggtgaggtgaggtgaggt 1317
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 DB 1378 ggtactggtgaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 1437
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 DB 1498 catgaacacaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggtgaggt 1557
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 DB 1558 ggcgtgtaagggagggagggagggagggagggagggagggagggagggagggagggagggaggg 1617
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QY 668 ccccttggtggcgacgagcggaagaagatgatactgacggatcaccaagagaagcc 727
 DB 1798 acccttggtggcgacgagcggaagaagatgatactgacggatcaccaagagaagcc 1854
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RESULT 14

ID ABL16432 standard; DNA; 3511 BP.
 XX ABL16432:
 AC 26-MAR-2002 (first entry)
 DT Drosophila melanogaster genomic polynucleotide SEQ ID NO 769.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmacological; gene; ds.
 KW Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-0509231.
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR New Isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 XX interactions -
 PS Claim 1; SEQ ID NO 769; 21pp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB16175), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB101840-AB16175).

CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 3511 BP; 994 A; 779 C; 803 G; 935 T; 0 other;

Query Match 10.5%; Score 227; DB 23; Length 3511;

Best Local Similarity 66.4%; Pred. No. 3.6e-42;

Matches 326; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

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DB 3021 ttttcttaaggggtcaacaagatacccggaatccgttgcgggtgaagaccttaacc 3080
OY 128 taccagctacctcgcccgagggaggtgagggagtttgagctctgcggagact 187
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OY 188 gaaccacacgaacatcgtcaagcttcttgcgggtgagagagcggcggaagcccgagaa 247
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DB 3141 caaccacgagaaatagtaagctgttgcgatacgagaggaatcaagggggtggtgttaa 3200
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DB 3501 cgatctctacg 3511
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RESULT 15

AAS27160 standard; cDNA; 538 BP.

XX AAS27160;

XX 07-NOV-2001 (first entry)

DE cDNA encoding novel signal transduction pathway protein, Seq ID 195.

XX Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
XX antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
XX Immune system disorder; rheumatoid arthritis; inflammatory condition;
XX organ transplant rejection; infection; hepatitis C; blood disorder;
XX sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
XX cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
XX reproductive system; gastrointestinal; liver disorder; AIDS; ss;
XX acquired Immune deficiency syndrome.

XX Homo sapiens.

XX WO200154733-A1.

XX

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PD 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01312.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
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PR 05-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232081.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 21-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
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DR P-PSDB;AAU17243.

PT Novel polypeptides useful for diagnosing, treating, preventing and/or

PT diagnosing disorders related to the proteins, including cancers, immune

PT disorders and neuronal disorders

PS Claim 1; SEQ ID NO 195; 880pp; English.

XX

CC The invention relates to novel isolated polypeptides (I), and

CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for

CC diagnosing, preventing and treating diseases including immune system

CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ

CC transplant rejections and graft versus host disease, infectious diseases

CC (e.g. hepatitis C), bleeding disorders, hemoglobin abnormalities and

CC other blood-related disorders (sickle cell anemia), myeloproliferative

CC disorders, primary haematopoietic disorders, hyperproliferative

CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative

CC abnormalities (Down syndrome), ischemic injury (e.g. stroke), renal

CC disorders (e.g. glomerulonephritis), cardiovascular disorders

CC (e.g. arrhythmia), respiratory disorders, dermatological disorders

CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.

CC Addison's disease), reproductive system disorders, gastrointestinal

CC disorders (inflammatory disorders), liver disorders (cirrhosis),

CC as stimulators of B-cell responsiveness to pathogens, activators of

CC T-cells, to induce higher affinity antibodies, and as a means to induce

CC tumour proliferation in pathologies e.g. acquired immune deficiency

CC syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction

CC pathway protein coding sequences and PCR primers of the invention.

XX

Query Match 8.3%; Score 178.2; DB 22; Length 538;

Best Local Similarity 63.5%; Pred. No. 2.9e-31;

Matches 287; Conservative 0; Mismatches 164; Indels 1; Gaps 1

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OY 241 ggcagaagttactgtgtatggaagtactctccagtggagacctgtgtgagtcgtcga 300

DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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OY 342 aaccttctaagcctatgactaccacagaatctgtaattcttatttgttttgagagtgg 401

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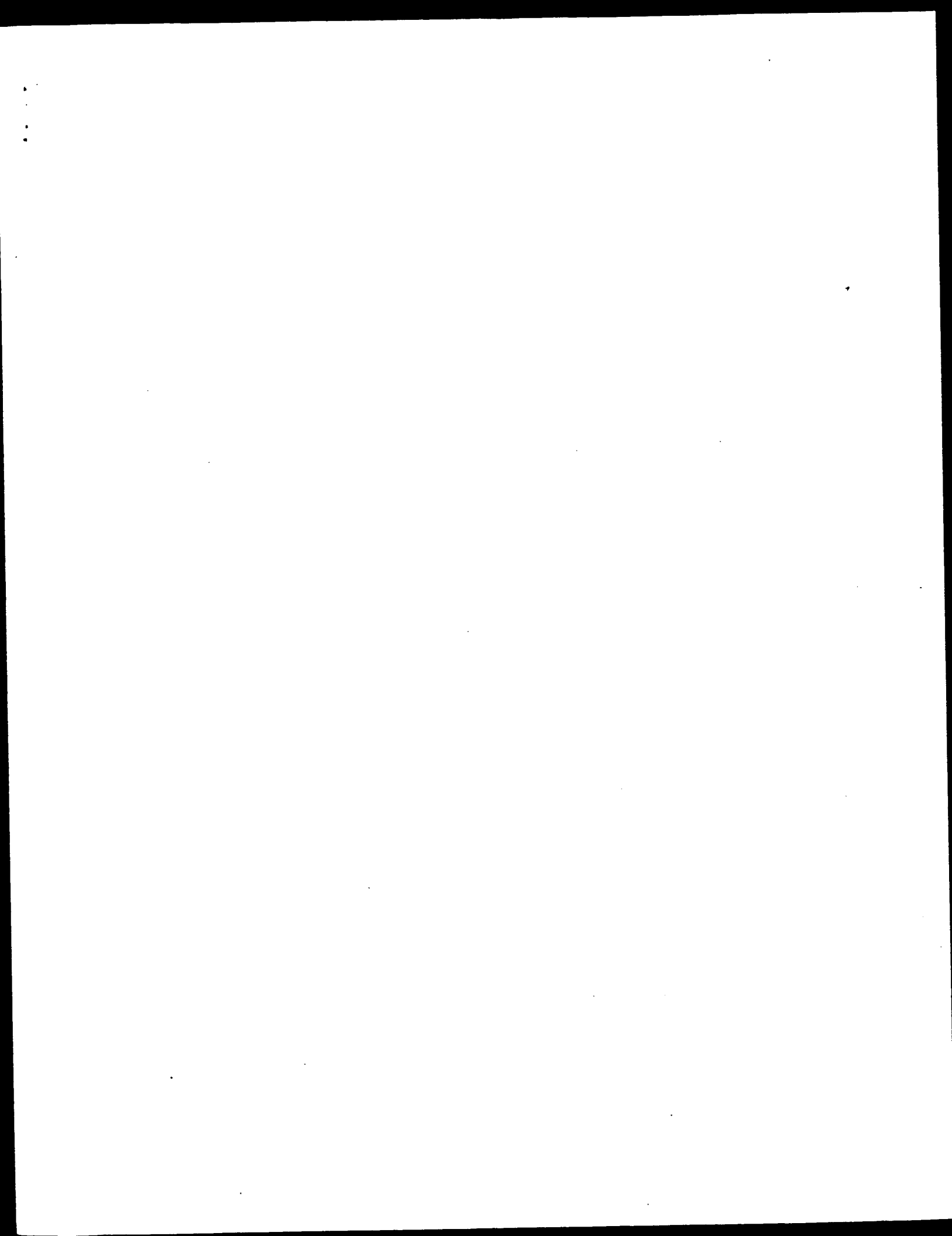
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 14, 2002, 12:20:07 ; Search time 147.27 Seconds

(without alignments)
3592.684 Million cell updates/sec

Title: US-09-582-397A-1

Sequence: 1 agatcagagagagagagcaat.....agcactcttgatgtctgag 2154

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	463.4	21.5	2994	2	US-08-812-533-1
3	87.8	4.1	2268	2	US-08-890-853-1
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5	87.8	4.1	2268	2	US-09-099-125A-1
6	87.8	4.1	2268	2	US-09-197-008-1
7	87.8	4.1	2268	4	US-09-032-476-1
8	87.8	4.1	2268	4	US-08-890-854-1
9	87.8	4.1	2268	4	US-09-023-324-1
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24	87.8	4.1	3966	3	US-09-215-131-1
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43	50.2	2.3	2273	4	US-09-168-629-1	Sequence 1, Appl1
44	50.2	2.3	2273	4	US-08-810-131A-1	Sequence 1, Appl1
45	49	2.3	2124	4	US-09-198-122-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-971-937-1
; Sequence 1, Application us/08971937
; Patent No. 5776717
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaoan
; TITLE OF INVENTION: TRAF2-Associated Kinase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentlin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,937
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/812,533
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: 797-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..2259
; US-08-971-937-1

Query Match 21.5%; Score 463.4; DB 1; Length 2994;
Best Local Similarity 59.08; Pred. No. 6.1e-106;
Matches 794; Conservative 0; Mismatches 551; Indels 0; Gaps 0;

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 DB 731 CATTTAGACCTTTGAAGGCTCTGTAGAGATTAAGAAATGATGTATTAATTAATTAATTA 790
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 DB 1091 ATAAACCAACCAAAATTTATTTCTTCAAAATTAAGAAATTAATTAATTAATTAATTAAT 1150

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RESULT 2
 US-08-812-533-1
 ; Sequence 1, Application US/08812533
 ; Patent No. 5837514
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Zhaodan
 ; TITLE OF INVENTION: TRAF2-Associated Kinase
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY IAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/812,533
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: T97-002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2994 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 73..2259
 ; US-08-812-533-1

Query Match 21.5%; Score 463.4; DB 2; Length 2994;
 Best Local Similarity 59.0%; Pred. No. 6, 1e-106;
 Matches 794; Conservative 0; Mismatches 551; Indels 0; Gaps 0;

QY 1 agatgcagagcagacgaattactgtgacacagatgacccctgctggggcagggccca 60
 DB 71 AGATGCAGAGCAGACGAACTTCAATCATCTGTGCTTTATCTGATTTTAAAGCCAAAGACCTA 130

QY 61 ctgcagtggtacaaagcccgcaacaagaatccgagagctggtgctgtgaagctc 120
 Db 131 CTGCAATATGTTTCGTGGAAGACATTAAGAACTGGATTTATTTCTATCAAGAT 190
 QY 121 tcaactaccagctacgtcgcccgaggtgcaggtgaggaagatcttgaagctcgc 180
 Db 191 TTAATTAACATTAAGCTTCCTGTCAGTGGATGTTCAATAGAGAAATTTGAAGTGTGA 250
 QY 181 ggaagctgaaccaccagaacatcgtaagctcttgcgtgaggaagagcgagcc 240
 Db 251 AAAAAGCTCAACCAAAAATTTGCTCAAAATTTGCTATGAGAGAGACACAAACAA 310
 QY 241 ggcgaaggaactggtgaggaactgctccagtgaggaagcctgctgagtgctgaga 300
 Db 311 GACATTAAGATCTTATATGGAATTTTGTCTGATGGAGATTATACACGTGTTTAAAG 370
 QY 301 ggcctgagaatgcttggagctgctgaggaatgagtcctggtggtgctgctgtg 360
 Db 371 AACCTTCAATGGCTTATGAGCTACCAAGATCTGAATTTGTTTGGAGATTTGG 430
 QY 361 tggcggcgaactgaaccactgaggaagagcattgctgacgcgacataagccggaga 420
 Db 431 TGGGTGAATGAATCACTACGAGAGAAATGATAGTGCACCGTGAATTCAGCAGGAA 490
 QY 421 acatcagcgcctcgtgaggaaggaaggaagcagcactcaagctgacagactcgagg 480
 Db 491 ATATCATGCGTGTATATGAGGGAAGATGAGACAGTCTGCTCAAACTCAACGATTTTGG 550
 QY 481 ctgcccggagagcgtgagatgagagaagtcgctcgtcgtctatgaggaactgagag 540
 Db 551 CACCTTAGAGATTAAGAAATGATGAGACAGTTGTTCTCTGTATGGCAGAGAAATAT 610
 QY 541 tgcacccagacatgataagacggcggtgcttgaagagcccgcaaaaagcgttcggag 600
 Db 611 TGCACCTGATATGATGAGAGAGACAGTCTTAAGAAAAGATCATGAGAAATATGAG 670
 QY 601 tgaacttgatctcgtgagcattgagccttgtaacatgacagcactgagcagctgc 660
 Db 671 CAACAGCTTGTATCTTGGAGCATGGGGTAAATTTTACATGACGATCTGATCTAC 730
 QY 661 ccttcaccccttggtagggcccgagcaagaagatcatgtaaccggaatcaccaag 720
 Db 731 CATTTAGACCTTTGAGAGGCGCTGTAGAGAAATGAAGATGATTAATAATTAACAG 790
 QY 721 agaagccggcgtgagcattgacaggtgcagagggcgaggaagcccgccgtgag 780
 Db 791 GAAGAGCTTCTGGTGAATATCTGAGGTACAGAAACAAATGAGCAATGACTGGA 850
 QY 781 gctacacccctcccatcacctcgcaagctgtaactggggctgagagccagctgtgcca 840
 Db 851 GTGAGACATGCTGTTTCTTGACGCTTTCGCGGGCTCTCAGGTTTACTTACCCCTG 910
 QY 841 tcttgcccaacatcctgtagggagtgaggaagcagagcgtgagggcttcgacagcttg 900
 Db 911 TTTCTGCAAAATCTTGTGAAGCAGATCAGGAAAGTGTGGGGCTTTTGAACGTTTTTT 970
 QY 901 cggagagcagtgacatcctgtagcagagtgctgctcatgtctctccctgcagggcag 960
 Db 971 CAGAAACTAGTATATCTTACCGAATGTAATTCATTTTTCGCTACCAACAAATGA 1030
 QY 961 tcttgacacacatctatatacctgcccacaacagatagcaatcttcagagagccgtg 1020
 Db 1031 CAGCTCATTAAGATTTATATACATACATTAATACGCTACTATATTTTCTGAACTGAT 1090
 QY 1021 acaagcagagcagtgtagcccccagcagaggaagtaaccttgaaggtacccctgtg 1080
 Db 1091 ATAAACAAACCAAAATTTATTTCTTCAAAATCAAGAACTTATCTACGAAGGGCAGCCTTAG 1150
 QY 1081 tcttgagagccagcgtctcagacagacatcgcccacagcagcgcaagcccccctga 1140
 Db 1151 TCTTAGAACCTTGGAAGGCTGAGCAACATTTCCCTAAAACTACTGAGAAACCTTATAT 1210
 QY 1141 cctcttcagcagcagcatcccttaaggggctgagccttcaggaagccctgtctgagctc 1200

Db 1211 TTGTAGTAACCGGGGAACTCTGATACATAGATTAATATGAAAAAATTTCCCTCC 1270
 QY 1201 ccaagtgctgctcccaagatgagctgagcaggtattacaactgcccagggcgtgtg 1260
 Db 1271 CTAAAGATACATCCACGTTATGATTAAGACGGGATGCTACAGGCTTAAGCAATTAACG 1330
 QY 1261 ggcggcgtacccagggccctcgagcagggccctgctggtatggcagagactaagt 1320
 Db 1331 GGGTGTGTGTATTTGCTGAGAAATGCCAGTACTTACTGCTTTATACGAATTAATGC 1390
 QY 1321 ttcggggcgtcagctggatcatgga 1345
 Db 1391 GAAAGGGATACGATGCGCTGATTTGA 1415

RESULT 3
 US-08-890-853-1
 Sequence 1, Application US/08890853
 Patent No. 5851812
 GENERAL INFORMATION:
 APPLICANT: Goeddel, David V.
 APPLICANT: Motorola, John
 TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/890,853
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-006-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2268 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-890-853-1

Query Match 4.1%; Score 87.8; DB 2: Length 2268;
 Best Local Similarity 50.5%; Pred. No. 1.5e-12;
 Matches 277; Conservative 0; Mismatches 257; Indels 15; Gaps 2;

QY 27 tggcacacagatgacgtgctgagggaagggccactgcccagtgtagtcaagagccgcgaac 86
 Db 43 TGGGAATGAAGAGCGGCTTGAGAGGAGGATTTGGAATGATGATGATGATGATGAT 102
 QY 87 aagaatccggaagcgtgctgctggtgaggtcttcaactaccagctaccctgagccc 146
 Db 103 CAGGAAGAGGTGAGACATTTGCTCAAGCAGTGGCCGAGAGCTCAGCCCGGAGAC 162
 QY 147 cgcgagtgctcaggtgaggaattgaggtctcctggaagcgtgaacccacacaaatcgtc 206
 Db 163 CGAGAGCGGTGTGCTCGAGATCCAGATTCATGAGAGGCTGAGCCCAACCCCAATGTGTG 222

Query Match	4.1%;	Score 87.8;	DB 2;	length 2258;
Best Local Similarity	50.5%;	Pred. No. 1.5e-12;		
Matches 277;	Conservative 0;	Mismatches 257;	Indels 15;	Gaps 2

Query Match	4.1%;	Score 87.8;	DB 2;	length 2258;
Best Local Similarity	50.5%;	Pred. No. 1.5e-12;		
Matches 277;	Conservative	0;	Mismatches 257;	Indels 15; Gaps 2

Query Match	4.1%;	Score 87.8;	DB 2;	length 2258;
Best Local Similarity	50.5%;	Pred. No. 1.5e-12;		
Matches 277;	Conservative	0;	Mismatches 257;	Indels 15; Gaps 2

QY 375 caactcgaggaagcagcattgtcatcgcagcatcaagccgagggaacatcatgcyctc 434
Db 403 TACCTTCATGAAACAGATCATCATCGGATCTAAAGCCAGAAAACATCTCTGAG 462
QY 435 gtaggaggaagggcagagcattctacaagctgacagacttcggcgctcccgagctg 494
Db 463 CAAGGAGAACAGAGTTA---ATACACAAATATTGACCTTAGATATGCCAAGAGCTG 519
QY 495 gatgatgatgaagltcgtcgtctctatgagactgaggaatctcatcccgacatg 554
Db 520 GATGAGGGCAGCTTTGGACATCATCTCGGGAGCCCTGCACTGACCTGCCCCAGAGCTA 579
QY 555 tatgagcgg 563
Db 580 CTGAGCAG 588

RESULT 9
US-09-023-324-1
Sequence 1, Application US/09023324
Patent No. 623513
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Cao, Zhaoan
APPLICANT: R. grier, Catherine
TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,324
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/890,854
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2268 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-023-324-1

Query Match 4.18; Score 87.8; DB 4; Length 2268;
Best Local Similarity 50.58; Pred. No. 1.5e-12;
Matches 277; Conservative 0; Mismatches 257; Indels 15; Gaps 2;

QY 27 tggagacaaagtgaacgctgctgggagcagggccatcgcagtgctcaagagccggcaac 86
Db 43 TGGGAAATGAAAGAGCCCTTGGGAGCAGGGGATTTGGAAATGTCATCCGATGACACAAAT 102
QY 87 aagaatcgcgagagcgtgtgtcgtgaaggtctcaaacactacagcttacctgagcc 146

Db 103 CAGGAACAGGTGAGCAGATTGGCCATCAAGCAGTGCAGGAGCTAGCCCCCGAAC 162
QY 147 cgcagagtgccaggggagaggaattgaggtcctcggaagctgaaccacagaaatcgtc 206
Db 163 CGAGGCGGCTGCTCGGAGATCCAGATCATGAGAAAGCTGACCCCAATGTGGTG 222
QY 207 aagctccttggtgaggaagcggcggaagccg-----cagaagtgctg 254
Db 223 GCTGCCCAAGATGTCCCTGAGGGGATGCAACTTTGGCGCCCAATGACCTGCCCTGCTG 282
QY 255 gtatgagactctctccagtgaggcctgtgagtgtgctgagagagccctgaagatgccc 314
Db 283 GCCATGAGTACTGCGAAGAGAGATCTCCGGAAGTACCTGAAACAGAGTTGANAAGTCC 342
QY 315 ttgggctgctgaggaatgaatctcgtgtgtctgctgctgtgtgtgtgtgtgtgtgtgt 374
Db 343 TGTGCTCTCGGGAAGGTCCATCTCACCTTCTGAGTGAATGCTGCTGCTGCTGCTGCTG 402
QY 375 caactcgaggaagcagcattgtcatcgcagcatcaagccgagggaacatcatgcyctc 434
Db 403 TACCTTCATGAAACAGATCATCATCGGATCTAAAGCCAGAAAACATCTCTGAG 462
QY 435 gtaggaggaagggcagagcattctacaagctgacagacttcggcgctcccgagctg 494
Db 463 CAAGGAGAACAGAGTTA---ATACACAAATATTGACCTTAGATATGCCAAGAGCTG 519
QY 495 gatgatgatgaagltcgtcgtctctatgagactgaggaatctcatcccgacatg 554
Db 520 GATGAGGGCAGCTTTGGACATCATCTCGGGAGCCCTGCACTGACCTGCCCCAGAGCTA 579
QY 555 tatgagcgg 563
Db 580 CTGAGCAG 588

RESULT 10
US-08-910-820-8
Sequence 8, Application US/08910820
Patent No. 6258579
GENERAL INFORMATION:
APPLICANT: Mercurio, Frank
APPLICANT: Zhu, Hengyi
APPLICANT: Barbosa, Miguel
APPLICANT: Li, Gnan
APPLICANT: Murray, Brian W.
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,820
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.413C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2271 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-910-820-8

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Query Match      4.1%; Score 87.8; DB 4; Length 2271;
Best Local Similarity 50.5%; Pred. No. 1.5e-12;
Matches 277; Conservative 0; Mismatches 257; Indels 15; Gaps 2;

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QY 27 tggcacacagatgacctgtctgggagcaggggacacatgctgacaaagcccgcaac 86
DB 43 TGGGAATGAAGAGCGCCCTGGGACAGGGGATTTGGAATGTCAATCCGATGGACAACT 102
QY 87 aagaatccggagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 146
DB 103 CAGGAACAGGTGAGAGATTTGCCATCAAGCAAGTGGCCGAGAGAGCTCAAGCCCGGAC 162
QY 147 cgcgaggtgacaggtgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 206
DB 163 CGAGAGCGGTGTGCTGTGAGATTCAGATCATGAGAAAGCTGACCCCAATGTGTGTG 222
QY 207 aagctcttgcggtggaagagacgagcggagcggg-----cagaaggtactg 254
DB 223 GCTGCCGAGATGTCCCTGAGGGGATGCAAGAACTTGCGGCCCAATGACCTGCCCTGTG 282
QY 255 gtgatgagatgactgtctccagttggaagcctgtgtgtgtgtgtgtgtgtgtgtgtgt 314
DB 283 GGCATGAGAGACGTCAGAGAGAGATCTCCGAGATACCTGAAACAGTTTGAACCTGC 342
QY 315 ttgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 374
DB 343 TGTGCTGTGCGGGAAGTGCATCTCACCCTTCTAGTACATTTGCCCTGTGCGTTAGA 402
QY 375 caactgcgaggaagacgagcattgtgtcatctcgacatcaagccggagagacatcatgtgcctc 434
DB 403 TACCTTCATGAAGAACAGAAATCATTCATCGGAGATCTAAAGCCAGAAACATGCTGTGAG 462
QY 435 gtatggagagagagagagagacatctcaagctgtcacagactgtgtgtgtgtgtgtgtgt 494
DB 463 CAAGGAGAACAGAGGTTA--ATACACAAATATTATTAAGCTAGATATGCAAGAGAGCTG 519
QY 495 gatgatgatgaagaatgcgtctgtctgtctgtctgtgtgtgtgtgtgtgtgtgtgtgtgt 554
DB 520 GATCAGAGGAGCGTCTTGGACATCATTCGTGTGAGGAGACCCGTGAGTACCTGAGGCCAAGAGCTA 579
QY 555 tatgagcgg 563
DB 580 CTGAGAGCAG 588

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RESULT 11
US-09-168-629-14
; Sequence 14, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: D'Donato, Joseph A.
; APPLICANT: Rothwarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: Zandi, Ebrahim
; TITLE OF INVENTION: Ikb kinase, Subunits thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 3295
; CURRENT APPLICATION NUMBER: US/09/168,629
; EARLIER FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,470
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2931

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(2306)
; US-09-168-629-14

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Query Match      4.1%; Score 87.8; DB 4; Length 2931;
Best Local Similarity 50.5%; Pred. No. 1.7e-12;
Matches 277; Conservative 0; Mismatches 257; Indels 15; Gaps 2;

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QY 27 tggcacacagatgacctgtctgggagcaggggacacatgctgacaaagcccgcaac 86
DB 78 tgggaatgaagagagcgtcttgggacaggggagatttgaatgcatccgattgtgcacat 137
QY 87 aagaatccggagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 146
DB 138 caggaacaaggttgacagattgtcatcaagcagatgcccggcagagagctcagcccggagac 197
QY 147 cgcgaggtgacaggtgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 206
DB 198 cgaagcgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 257
QY 207 aagctcttgcggtggaagagacgagcggagcggg-----cagaaggtactg 254
DB 258 gctgcgcgagatgtctccctgagggagtgacagactgtgtgtgtgtgtgtgtgtgtgtgtgt 317
QY 255 gtgatgagatgactgtctccagttggaagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 314
DB 318 gcaatgagagatgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 377
QY 315 ttgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 374
DB 378 tgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 437
QY 375 caactgcgaggaagacgagcattgtgtcatctcgacatcaagccggagagacatcatgtgcctc 434
DB 438 taccttcattgaagaacagatcatcatcatcgagatctaaagcagaacatcgtctctgag 497
QY 435 gtatggagagagagagagacatctcaagctgtcaagactgtgtgtgtgtgtgtgtgtgtgtgtgt 494
DB 498 caagagagacagagttt--atacaaaaatlatgtgacctagatagatagcaagagagctg 554
QY 495 gatgatgatgaagaatgcgtctgtctgtctgtctgtgtgtgtgtgtgtgtgtgtgtgtgt 554
DB 555 gatcagggcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 614
QY 555 tatgagcgg 563
DB 615 ctgagagcag 623

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RESULT 12
US-09-215-131-1
; Sequence 1, Application US/09215131
; Patent No. 6030834
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK Beta Regulates Transcription Factors
; FILE REFERENCE: 1449.002
; CURRENT APPLICATION NUMBER: US/09/215,131
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3966
; TYPE: DNA
; ORGANISM: human
; US-09-215-131-1

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Query Match	4.1%;	Score 87.8;	DB 3;	length 3966;
Best Local Similarity	50.5%;	Pred. NO. 1.9e-12;		
Matches 277;	Conservative 0;	Mismatches 257;	Indels 15;	Gaps 2

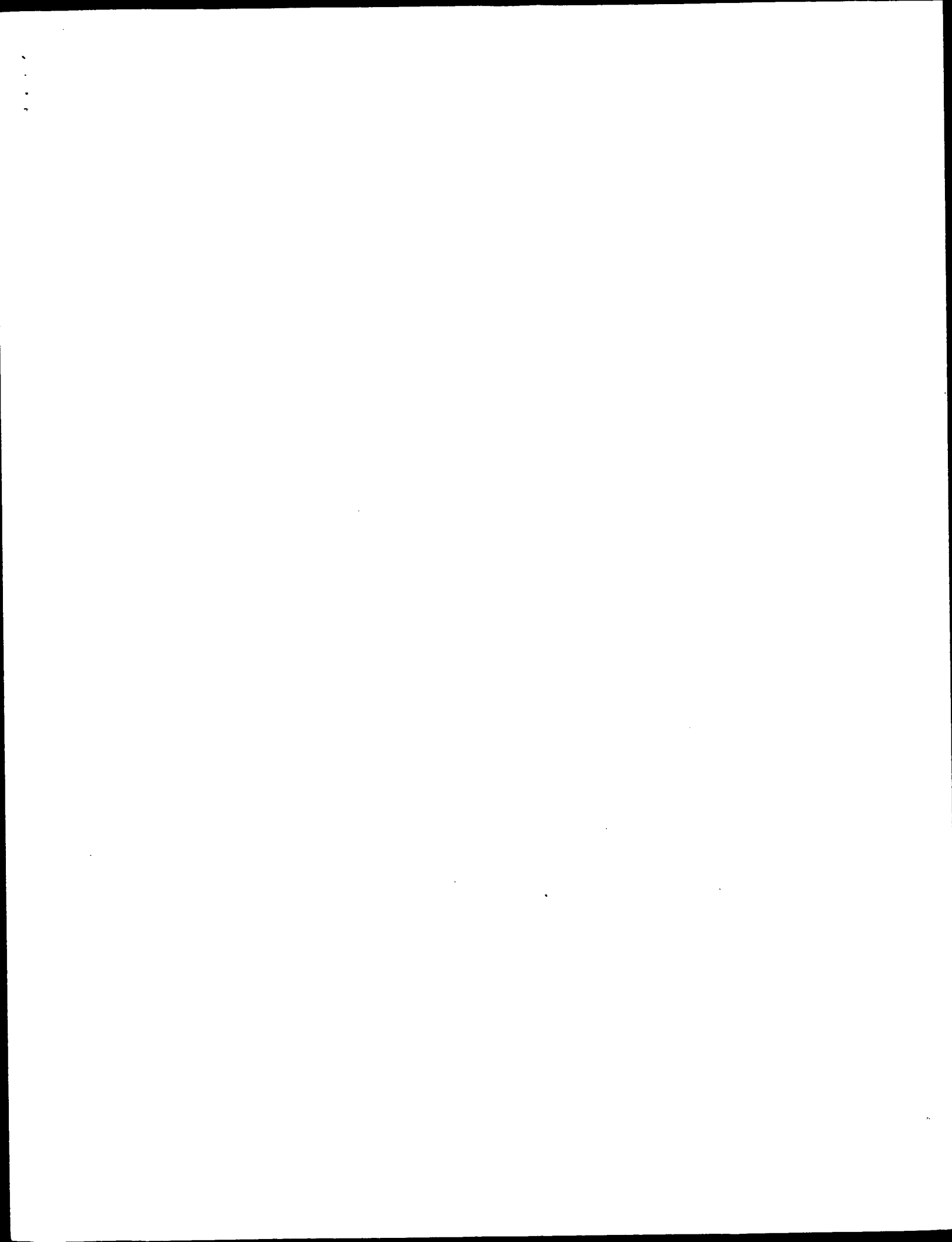
RESULT 14
US-09-124-476-1
Sequence 1, Application US/09124476
Patent No. 6087169
GENERAL INFORMATION:
APPLICANT: MICHALOVICH, DAVID
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,476
FILING DATE: 29-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 97305868.8
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul P
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30498
TELECOMMUNICATION INFORMATION:

Wed May 15 09:30:36 2002

us-09-582-397a-1.rml

Page 11

Search completed: May 14, 2002, 17:31:08
Job time: 18661 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2002, 14:41:43 ; Search time 5236.03 Seconds
(without alignments)
5552.382 Million cell updates/sec

Title: US-09-582-397a-1
Perfect score: 2154
Sequence: 1 agatgcagagcacagcaat.....agcactctgctgtctgag 2154

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: em_estln:*
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8: em_hic:*
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12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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4	652.8	30.3	656	10	BG248299 602400335
5	630.6	29.3	858	10	BM051314 603634307
6	621.6	28.9	867	10	BG420333 602448354
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8	526.6	24.4	871	9	AL553975
9	479.6	22.3	505	9	AI904078 MR-BT041-
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11	428	19.9	474	9	AM175691 OYO-BT004
12	415.8	19.3	566	10	BM089043 502687 MA
13	382.6	17.8	723	10	BI226990 602952136
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15	382	17.7	533	10	BE305681 601101283
16	381	17.7	562	10	BF191384 238954 MA
17	378.4	17.6	998	10	BE396447 601289358

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23	349	16.2	537	9	AI806295
24	348	16.2	539	10	BI342138
25	346	16.1	616	9	BE200581
26	343.8	16.0	347	10	BF930112
27	336	15.6	501	9	AM266810
28	333.4	15.5	679	10	BE544415
29	325.8	15.1	562	10	BI882863
30	323.4	15.0	332	9	AM402016
31	322.8	15.0	574	10	BI884083
32	321.4	14.9	504	9	AA827664
33	318.4	14.8	624	9	AM320459
34	316.2	14.7	556	10	BI344736
35	313	14.5	593	10	BE513758
36	309.4	14.4	470	9	AA909185
37	300.4	13.9	492	9	AA829237
38	291	13.5	487	10	BF736569
39	289.8	13.5	623	10	BG641584
40	288.8	13.4	360	9	AM430086
41	282.8	13.1	565	10	BI881724
42	281.4	13.1	573	9	AM323811
43	272.2	12.6	664	10	BE912896
44	268	12.4	498	9	AA919008
45	267.2	12.4	669	9	BB653341

ALIGNMENTS

RESULT 1
LOCUS BG754709 1031 bp mRNA linear EST 15-MAY-2001
DEFINITION 602714467P1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4854545 ,
mRNA sequence.
ACCESSION BG754709
VERSION BG754709.1 GI:14065362
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1031)
NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L10C1702 row: f column: 18
High quality sequence stop: 762.
Location/Qualifiers
1..1031
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4854545"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pORF7, Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(C). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling

FEATURES

source

Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT 222 a 319 c 319 g 169 t 2 others
ORIGIN

Query Match 33.8%; Score 728.8; DB 10; Length 1031;
Best Local Similarity 98.6%; Pred. No. 2,2e-142;
Matches 766; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

Qy 685 ggcggaaagaagatcatatgaccggatcacacagaagacggcgtgagccattgcaag 744
Db 1 ggcggaaagaagatcatatgaccggatcacacagaagacggcgtgagccattgcaag 60
Qy 745 gtgcacagagcgagagaagacggcgtgagccattgcaag 804
Db 61 gtgcacagagcgagagaagacggcgtgagccattgcaag 120
Qy 805 agctgtacatgagcgagagacggcgtgagccattgcaag 864
Db 121 agctgtacatgagcgagagacggcgtgagccattgcaag 180
Qy 865 agcagagcagatgagcgagagacggcgtgagccattgcaag 924
Db 181 agcagagcagatgagcgagagacggcgtgagccattgcaag 240
Qy 925 gactgtgtcatatgcttctcctgtccagagcagcctgacacacatctatcatg 984
Db 241 gactgtgtcatatgcttctcctgtccagagcagcctgacacacatctatcatg 300
Qy 985 ccccaacacagatagcatttccagagagcggtgacaaagcagcagatgtgccc 1044
Db 301 ccccaacacagatagcatttccagagagcggtgacaaagcagcagatgtgccc 360
Qy 1045 gacacagagatgcttctgagagcagcctgtgtccagagcagcagcagcagc 1104
Db 361 gacacagagatgcttctgagagcagcctgtgtccagagcagcagcagcagc 420
Qy 1105 agacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1164
Db 421 agacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
Qy 1165 agggagcgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 1224
Db 481 agggagcgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 540
Qy 1225 tgcagagcgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 1283
Db 541 tgcagagcgtgagcagcagcagcagcagcagcagcagcagcagcagcagc 600
Qy 1284 ctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1343
Db 601 ctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 660
Qy 1344 gaggctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1401
Db 661 gaggctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 720
Qy 1402 acctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1458
Db 721 acctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 777

RESULT 2
LOCUS BM051210 851 bp mRNA linear EST 07-NOV-2001
DEFINITION 603634157F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:5424662 5',
ACCESSION BM051210
VERSION BM051210.1 GI:16780477
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 851)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
Plate: LNCM1886 row: a column: 15
High quality sequence stop: 817.

FEATURES
source
1. 851
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5424662"
/clone.lib="NIH_MGC_43"
/tissue.type="normal pigmented retinal epithelium"
/lab.host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOB7; Site_1: XhoI; Site_2:
BclRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library. 1"

BASE COUNT 188 a 203 c 298 g 162 t
ORIGIN

Query Match 32.8%; Score 707.2; DB 10; Length 851;
Best Local Similarity 94.6%; Pred. No. 6.8e-138;
Matches 808; Conservative 0; Mismatches 38; Indels 8; Gaps 7;

Qy 55 gggccactgcccagtggtgtaacagcccgcaacaataccgagagctgtgtgta 114
Db 1 gggccactgcccagtggtgtaacagcccgcaacaataccgagagctgtgtgta 60
Qy 115 aggttttaacactaccagctactctgcccgcgaggtgcaagtgaggaattgag 174
Db 61 aggttttaacactaccagctactctgcccgcgaggtgcaagtgaggaattgag 120
Qy 175 tccctggaagctggaacacacagacacatcgtcaagctcttgcgtggaagagcg 234
Db 121 tccctggaagctggaacacacagacacatcgtcaagctcttgcgtggaagagcg 180
Qy 235 gaagcccgagagaagtgactggtgagtgactctcagctgaggaagcctgtgagtg 294
Db 181 gaagcccgagagaagtgactggtgagtgactctcagctgaggaagcctgtgagtg 240
Qy 295 tggagaagcctggaagatccttgggctgctgaggaatgagttccgtgtgtgct 354
Db 241 tggagaagcctggaagatccttgggctgctgaggaatgagttccgtgtgtgct 300
Qy 355 gtgtgtgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 414
Db 301 gtgtgtgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
Qy 415 cggggaacatcatgcccctgtagggagagagcagagcagcagcagcagcagcagc 474
Db 361 cggggaacatcatgcccctgtagggagagagcagagcagcagcagcagcagcagc 420
Qy 475 tcggcgtgcccggagctgtagatgaggaagttcgtctggtctatgaggaactgag 534

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LICM1231 row: e column: 10
High quality sequence stop: 647.

FEATURES

source
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/clone_lib="NIH_MGC_15"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

BASE COUNT 131 a 219 c 186 g 120 t

ORIGIN

Query Match

Best Local Similarity 99.7%; Score 652.8; DB 10; Length 656;
Matches 654; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES

source

1. .858
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5424961"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. 1"

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Plate: LICM186 row: n column: 02
High quality sequence stop: 733.

RESULT 5
BM051314 858 bp mRNA linear EST 07-NOV-2001
LOCUS 603634307P1 NIH_MGC_43 Homo sapiens CDNA clone IMAGE:5424961 5', mRNA sequence.
DEFINITION
ACCESSION BM051314
VERSION BM051314.1 GI:16780581
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 858)
REFERENCE
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC

Db 541 CTACCCCTCTTTCAGCAGCAGCCTTCTAAGGAGGCTGGCTTTCAGGACCTCTTGAC 600
Qy 1197 gtcccaagtcgtccccaagtgaaccctgcagagcgagattacaacatgcagagg 1252
Db 601 gtccccaagtgtgtctccccaagtgaaccctgcagagcgagattacaacatgcagagg 656

BASE COUNT 180 a 225 c 291 g 162 t

ORIGIN

Query Match 29.3%; Score 630.6; DB 10; Length 858;
Best Local Similarity 95.8%; Pred. No. 7.5e-122;
Matches 691; Conservative 0; Mismatches 24; Indels 6; Gaps 4;

Qy 597 ggggtgactgtagctctgtagcattgtagtcttaccatgacacactgtagc 656
Db 1 GGGGTGACTGTGATCTCTTGAGCATTTGAGTACCTTGTACCATGACCCACTGGCAGC 60
Qy 657 ctgacctcatccctcttgtaggacagcgagaaagagatcatgtaccgagatcac 716
Db 61 CTGCCCCCTTCACTCTTGTGTGGGCGACGGCGGAGAACAGATCATGTACCGGATCAC 120
Qy 717 acagagaagccgctgtaggacattgtagtgcacaaagcgagagagagagccctgtag 776
Db 121 ACGGAAGAGCGGCTGGGCGCATTTGCAAGTGTCCCAAGAGCGGAGAACCGCCCTGGAG 180
Qy 777 tggagctaacacctcccatcactgtagcagctgtcactgtaggctgtagagcagctgtag 836
Db 181 TGGAGCTACACCTCCCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 837 cccatcctgtagcaatcctgtaggagtgtagcagagcagagtgctgtagcagatgc 896
Db 241 CCCATCTCTGGCAACATCTCTGAGGTGAGCAGGCCCAAGTGTGGGCTTTCAGCAC 300
Qy 897 ttgtaggaagcagtagacatcctgtagcagagtgtagtctgtagtcttccctgtag 956
Db 301 TTGCGGAACACAGTACATCTCTGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Qy 957 gaagtcctgtagcaatcctgtagcagagtgtagcagagtgtagcagagtgtagcag 1016
Db 361 GGAAGTCTGACACATCTATATTCATGCGCCACACACAGATGAGCATTTTTCAGAGAG 420
Qy 1017 gtgacacagcagacagtgtagcctcccgagacagagagtagctctttagagtgtagc 1076
Db 421 GTGCAACAAACAGACAGTGTGCCCCCGACACAGAGTACCTCTTTCAGAGGTACCTC 480
Qy 1077 tgtgtcctcagagcagagtgtagcagacagacatcgcccaagcagagcagagcagc 1136
Db 481 TGTGTCTCTGAGACCGAGCTCTCAGCAGACAGCATGTGCGCCACAGACGAGAGCGCC 540
Qy 1137 ctgacctctttagacagacatccctaaagggtgtagcctttagagcagcctgtagc 1196

Qy 19 attaccgtgtagcagacagtagactgctgtaggagcag-ggggcaactgcagtgtagca 76
Db 2 ATTACCTGTGGCAACAGATGACCTGCTGGGCGCAGTGTGGGCGCACCTGCAAGTGTG 61
Qy 77 ggcgcgaacaagaatcgcgagagcgtgtagtctgtagaagtgcttcaacactcagagta 136
Db 62 GGCCCGCAACAAGAAATCCGAGAGCTGTGCTGTGTAAGGTCTTCAACACTACAGCTA 121
Qy 137 cctgtagcctcccgagagtgtagagtgtagagtgtagagtgtagagtgtagagtgtag 196
Db 122 CCTCGGCGCCCGGAGGTGAGGTGAGGAGTGTGAGGTCTCTCGGAGGTGAGACCA 181
Qy 197 gaacatgtagagtgcttctgtagttagagagagcagagcagagcagagtagtagt 256

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Oy	257	gatggagatcagctctccatctggagagcctctgagtgtctgtgaaagacccctggaaatgcctt	316
Db	242	GATGGAGATCAGCTCTCCATCTGGAGAGCCTCTAGTCTGTGGAGACCCCTGGAAGAGCCCTT	301
Oy	317	tggagctgcctgaagatgagttccctggctgtgctgcctgcctgctgtgtgtgtgcgcgcataaccca	376
Db	302	TGGGCTGCCCTGAGATGAGTTCCTGGTGTGCTGGCTGTGTGTGTGGCTGGCCGATTAACCA	361
Oy	377	ccctgcggagaaagcgcatctgtgcatctgcgaacatcaagccggggaaacatcatgcccctgt	436
Db	362	CCTGCGGAGAAAGCGCATCTGTGCATCGGACATCAAGCCGGGGAACATCATGCGCCTCGT	421
Oy	437	aggggaggaaggaggagacatctataaagcttcaagaactctgcgcgtctgcgcggaggagctga	496
Db	422	AAGGAGAGAGAGGGCGACAGACATCTACAAGCTGACAGACTTCGGCGCTGCCCGGAGACTGGA	481
Oy	497	tgatataagaagaatctgctctcgtctcgtctatctatggagactgaagagtaactgcatcccgatgla	556
Db	482	TGATATATAGAAAGTTCGTCCTCGCTCTATGGGACTGAGAGATACCTGCATCCCGACATGTA	541
Oy	557	tgaaggggcgcgtgtgctctgaaagccccaagaacgcttcgg-aggctgtgtgagatcct	615
Db	542	TGAGCGGGCGGTGCTTCCAAAGCCCCAGAAAGAAAGCTTCGGCGGTGATGTGGATCTCT	601
Oy	616	ggaagcatctgagtgacccctgttaccatctgagcaactctgagacccctgtccctcatcccttly	675
Db	602	GGAGCATTTGGAATGACTGACTTGTACATGACAGCAGCTGGAGCCTTGACCTTCATCCCTCATG	661
Oy	676	gtggagccacgcgcggagacaagaagatcatgct---accgatatccacacagaagaagccggcty	732
Db	662	GTGGGCGCACGTCGGACACAGAGACTCATGTAAACCGGATCAACCGGAGACCGGAGAACCGG	721
Oy	733	g 733	
Db	722	G 722	
RESULT	6		
LOCUS	BG420333	867 bp	mRNA linear EST 14-MAR-2001
DEFINITION	602448354P1 NIH_MGC_14 Homo sapiens cDNA IMAGE:4587013 5',		
ACCESSION	BG420333		
VERSION	BG420333.1	GI:13326839	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 867)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: rsraus@nhi.nih.gov Tissue Procurement: DCTD/DMR cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov plate: L1CM1316 row: k column: 14 High quality sequence stop: 662.		
FEATURES			
source			Location/Qualifiers 1..867

[illegible]

QY 301 gccctgagaatgctcttgagctgaggaatgagatctcctgagtgagctgagtgag 360
 DB 413 ACCCGTCAATGCTGATGAGTATGCAAGATATGCAATTTCTGCTTACAGATGTCG 472
 QY 361 tggcggcgaatgaac 420
 DB 473 TGGGGGGGATGATATCTCCGAGAGAACGGCATAGTGCACGAAATTTCAAGCCAGG 532
 QY 421 acatcatgagctcgttagagagagagagagagagacatcacaagctgacagctcgag 480
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 QY 481 ctgagcggagctgagatgagatgagatgagatgagatgagatgagatgagatgag 540
 DB 593 CCGCTCGAGAGCTGGAG 652
 QY 541 tgcacccgacatgtag 600
 DB 653 TGCATCCGAGCATGTATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 712
 QY 601 tgaactgagatctctgagagacatgagatgagatgagatgagatgagatgagatg 660
 DB 713 CTACCGTTGATCTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAG 772
 QY 661 cctcatccctcttgag 720
 DB 773 CGTTTACAGCTTTCGAG 832
 QY 721 aagaagcagctgag 780
 DB 833 GGAAGCGGCTGTGAGAGATGTGAGAGATGTGAGAGATGTGAGAGATGTGAGAGATGT 892
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 DB 893 GTGAGAGACATGCT 952
 QY 841 tccctgagacacatcctcctcctcctcctcctcctcctcctcctcctcctcctcct 900
 DB 953 TTTCTTCAACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1012
 QY 901 cggagagcagctgag 960
 DB 1013 CAGAGACAGTGTGAGAGATGTGAGAGATGTGAGAGATGTGAGAGATGTGAGAGATGT 1072
 QY 961 tccctgagacacatcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1020
 DB 1073 CGGCGCATTAAGATTTTCAATTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTT 1132
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 DB 1133 ATTAACCAACCAAGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1192
 QY 1081 tccctgagacacatcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1140
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 QY 1201 ccaagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1260
 DB 1313 CTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1372
 QY 1261 ggcgcgcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1320
 DB 1373 GGGTTTGTGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACG 1432
 QY 1321 ttcgagagctgag 1375
 DB 1433 GAAAGGGGAG 1492

QY 1376 -----ggaagtggcagaagacatccctcctcctcctcctcctcctcctcctcctc 1428
 DB 1493 AGAAGAGGAG 1552
 QY 1429 ggttc-----agcagctgctgagagagagagagagagagagagagagagagagag 1482
 DB 1553 AAGGTATGAG 1612
 QY 1483 aactgagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1542
 DB 1613 ACATACACACCAAGCTGCTGAGACTTTTCCAGTTTCCAGGAGAACATTAAGAACAGTCTTC 1672
 QY 1543 cggagagcccaag 1602
 DB 1673 AGGACATCAGCAGCAGCTGCTCCAGGGGCTTCTGCTGCGAGACCTGGGACATCAAG 1732
 QY 1603 ta-----catgag 1653
 DB 1733 AAGGACGATCCAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1792
 QY 1654 actcatcacaagctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1713
 DB 1793 CAGAGATTTACTATCATGTTCAAAAAGACAAAGACAGAGAGAGAGAGAGAGAGAGAG 1852
 QY 1714 agcagatcacaagctgagatagatgagatgagatgagatgagatgagatgagatgag 1773
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 QY 1774 tgtccag 1833
 DB 1913 ACTTCTCAAG 1972
 QY 1834 tgaaggtgctgag 1865
 DB 1973 TGAGAAAGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2004

RESULT 8
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 LOCUS AL553975 LTI.NFL006.PL2 Homo sapiens cDNA clone CS01079YB05 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL553975
 VERSION AL553975.1 GI:12894313
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 871)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 source
 1..871
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS01079YB05"
 /clone_1b="LTI.NFL006.PL2"
 /tissue="type="Placenta"
 /note="Vector: pCMVSPORT 6; Site: 1; NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 life technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :

BASE COUNT	http://fulllength.invitrogen.com"			
ORIGIN	200 a	222 c	294 g	151 t
				4 others

Query Match	24.4%;	Score 526.6;	DB 9;	Length 871;
Best Local Similarity	98.5%;	Pred. No. 4.6e-100;		
Matches 537; Conservative	4;	Mismatches 3;	Indels 1;	Gaps 1;

[illegible]

	RESULT	9		
	LOCUS	AJ904078/c		
	DEFINITION	MIR-6704l-1-220199~020 BTU04I Homo sapiens cDNA, mRNA sequence.	505 bp	mRNA linear EST 30-MAR-2000
	ACCESSION	AJ904078		
	VERSION	AJ904078.1		
	KEYWORDS	GI:6494465		
	SOURCE	EST.		
	ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.E., Matsushima, A., Bala, G.S., Simpson, D.H., Brustein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, ' M.J.', Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7),	3491-3496	(2000)
MEDLINE	20202663			
COMMENT	Contact:	Simpson A.J.G.		

Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPERSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
[http://www.ludwig.org.br/seq/gethtml.pl?cl=MGst2-MR-BT041-020.html](http://www.ludwig.org.br/seq/gethtml.pl?cl=MGst2-MR-BT041-020.html&cl=220199&cl=1)
 &cl=220199&cl=1)
 Seq primer: puc 18 forward.
 Location/Qualifiers
 1..505

BASE COUNT	102 a	155 c	147 g	100 t	1 others
ORIGIN					

Query Match	22.38;	Score 479.6;	DB 9;	Length 505;
Best Local Similarity	98.20;	Pred. No. 2.5e-90;		
Matches 496;	Conservative 0;	Mismatches 5;	Indels 4;	Gaps 1;

QY	488	ggagcctggatctgtagtggaaagcttcgcttcggtcctatggagactggagagtaacct-----gc	54.3
Db	505	GNAGCTGAGTATGATGATGAGAAAGTTCCGTCTCGCTCTATGGAGACTGAGAGATACCTGTGGCC	44.6
QY	544	atcccgacatgtaataagacgagcgagtgctctgaaagaccaccagaaaaagcgttcgaggtga	60.3
Db	445	ATCTTACATATGATATAGAGGCGCGGTGCTTGGAAAGGCCACGCAAAAAGCGTTCCGGGGTGA	38.6
QY	604	ctgtgatctctggagacattgagtagaccttgtaacatgacacatgagccttgacct	66.3
Db	385	CTGTGATATTCTGGAGGCAATTGGAGTGAACCTTTGATCAATCAACCAACTGGACGCTGCCT	32.6
QY	664	tcaatccctcttggatgggacacgagcggacaagaagatacaatgacggatcaaccaagaaga	72.3
Db	325	TCAATCCCTCTTTGATGGGCGCAAGCGCGCAACAGAGATCATGTACCGGATACCAACGGAGA	26.6
QY	724	agccggccttgggggacattgacagatggcccaagagggaggaagaagcgcccttgagtggagct	78.3
Db	265	AGCGGAGCTGGGGCAATGTCAAGATGTCCTCCAGAGGGGGGAAGAACAGGCCCTCTGGATGGAGCT	20.6
QY	784	acaacccctcccaatacaactctgcacgtgtgcaatgtgggtctgcaagacacgtctgtagcccaatc	84.3
Db	205	ACACCTCTCCCATCACTGCGACGCTGTCACTGGGGCTGCAAGACCAAGCTGGTGGCCATTC	14.6
QY	844	tggcaaaactcttggaagtggaagcaagatgctgggggtctggaacgaatctcttgagg	90.3
Db	145	TGGCAAACTCTTGGAAGTGGAGGACCAAGTGTGGGGCTTCCACACAGTTCTTTTCCGG	8.6
QY	904	agaccagtgagacatcctgcaagagagttgtcgtccatgctctctcctgtcccaagcaatcc	96.3
Db	85	AGACCAAGTACATCCTGCAAGGATTTGTGTCATATGTCTTCCCTGTGCCAGGCAATTC	2.6
QY	964	tgcacacatctatatatcatgcccga	98.8
Db	25	TGCAACACATCTATATCCATGGCCA	1

RESULT 10
BF073571

LOCUS BF073571 558 bp mRNA linear EST 25-APR-2001
 DEFINITION 220312 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BF073571
 VERSION BF073571.1 GI:10867082
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 558)
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
 Caas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
 G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A., Chitko-McKown, C.G.,
 Perle, G., Holt, T., Karamycheva, S., Liang, F., Quackenbush, J. and
 Keefe, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 COMMENT
 TITLE
 JOURNAL
 MEDLINE
 CONTACT: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt-trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -m1nscore 18
 and -minmatch 12 options.
 PCR primers
 FORWARD: AGGAACAGCTATGACCAAT
 BACKWARD: GTTTCACAGTACGACG
 Plate: 79 ROW: P COLUMN: 10
 Seq primer: ATTGAGTACACTATAG.
 Location/Qualifiers
 1..558
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 2BOV"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Library made from pooled tissue from testis, thymus,
 semitendinosus muscle, longissimus muscle, pancreas,
 adrenal, and endometrium."

BASE COUNT 111 a 157 c 198 g 92 t
 ORIGIN
 Query Match 21.5%; Score 463.6; DB 10; Length 558;
 Best Local Similarity 89.4%; Pred. No. 5.9e-87;
 Matches 499; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
 Oy 105 gtgtgtgtgaaggtctcaactaccagctacgtcgccgcgagtgtagtgag 164
 Db 1 GTTGTGTGAAGGTGTGAACGCGGCTACTAGCGCCGCA3GTGAGTGAAG 60
 Oy 165 gatttgaggtctctggaagctgaaccacacagatcgtcagctcttggtggtgag 224
 Db 61 GAATTGAGGTCTCTGCGGAAGCTGAACATCAATCAAGCTTTCCGGGTGAG 120
 Oy 225 gagaagcgaggaagcgaggaagtgtagtgagtgagtgagtgagtgagtgag 284
 Db 121 GAGACGGGCGCGCGCGCGAGAGTGTGTGATGAGTGTGTCGACGCGGAGCTG 180
 Oy 285 ctgagtgtagtgagagccttgagatgcttggtggtggtgagtagtgagtgag 344
 Db 181 CTGAGCTGTGTGAGAGCCCGGAGAACGCTTGGGCTGCGGAGACGAGTTCCTG 240
 Oy 345 gt 404
 Db 241 GTGCTGTGCTGTGCTGTGCGCGCGGAGTGAACCTGCGGAGAGACGATGTCAC 300

Oy 405 gacatcaagcgagggaacatcatcgctcgtagggagggagggagagcatcaag 464
 Db 301 GACATCAAGCGCGGAGAACATCATCGCTGTGGGCGAGAGGCGGACATCTACAA 360
 Oy 465 ctgagagcttcggtcggtcggtcggtcggtcggtcggtcggtcggtcggtcg 524
 Db 361 CTGAGTACTTGTGGGGCGCGCGGAGAGTGTGAGAGCGAGAAAGTTGTCTCAT 420
 Oy 525 gggactgagaggtacatcatccagacatgtagagggcggtgcttcgaagcccg 584
 Db 421 GGCACCGAGAGTACTCTGACCTGACATGTACGAGCGGCGAGTCTTCGCAAGCC 480
 Oy 585 caaaaagcttcgggtgagtgtagtctctgagagcatgtagagtgtagtgag 644
 Db 481 CAGAAAGCTTTGGGGTGTGATCTGTGATCTGTGAGACATCGGGGTGACCTGAC 540
 Oy 645 gccactgagctgccc 662
 Db 541 GCCACCGAGCTGCC 558

RESULT 11
 LOCUS AM175691 474 bp mRNA linear EST 16-NOV-1999
 DEFINITION QV0-BT0041-090999-018-b08 BT0041 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AM175691
 VERSION AM175691.1 GI:6441637
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 474)
 Email: asimpson@ludwig.org.br
 HCGP http://www.ludwig.org.br/ONESTES.
 The FAPESP/LICR Human Cancer Genome Project
 Unpublished (1999)
 JOURNAL
 COMMENT
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0-BT0041-
 090999-018-b08&t3=1999-09-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 129
 High quality sequence stop: 416.
 Location/Qualifiers
 1..474
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="BT0041"
 /dev_stage="Adult"
 /note="organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ONESTES PCR (U.S. Letters Patent application No. 196
 716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT 101 a 127 c 161 g 85 t
 ORIGIN
 Query Match 19.9%; Score 428; DB 9; Length 474;
 Best Local Similarity 96.8%; Pred. No. 1.6e-79;
 Matches 459; Conservative 0; Mismatches 10; Indels 5; Gaps 2;
 Oy 412 agccggggaacatcatcgctcgtagggagggagggagagagcatcaagctgacag 471

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM951 row: 9 column: 09
 High quality sequence stop: 674.

FEATURES

Location/Qualifiers
 1. 723

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5096480"
 /clone_1ib="NIH_MGC-8"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lymph. Vector: pORF7. Site: 1: XhoI; Site: 2:
 EcoRI; CDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAC(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT

165 a 193 c 240 g 125 t

ORIGIN

Query Match

Best Local Similarity 17.8%; Score 382.6; DB 10; Length 723;
 Matches 418; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

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OY 1 agatgagagacagacgaattactctgtgacacagatgactgtgagcagggagca 60
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DB 300 AGATGAGAGACACAGCAATTAACCTGTGCACACAGATGACCTGTGGGAGGGGCA 359
OY 61 ctgccagtggtacaagagccgcaacaagaatccgagagagctgtgtgtgaagctc 120
    |||||||
DB 360 CTGCCAGTGTGTCAAGGCCGCCGACACAGAAATCCGAGAGCTGTGTGTGAAGTCT 419
OY 121 tcaaacctaccagctactctgcgcccgcgaggtgcaaggttgaagctctgc 180
    |||||||
DB 420 TCACACTACACAGCTACCTGCGG-CGCCGAGAGTGAAGTGAAGTGTGAGTCTGC 478
OY 181 ggaagctgagacacacgaacatcgtcaagctcttgcggtgagagagcgggagagc 240
    |||||||
DB 479 GGAAGCTGAAACCAACGAAATCCTGTAAGTCTTGTGCGTGAAGAGAGAGCGGACCC 538
OY 241 ggcagaaggtactgtgtagtactctccagtgagagcctgtctgtgtgtgtgagga 300
    |||||||
DB 539 GGCAGAGGTACTGTGATGAGTACTGCTCAGTGGGAGCTCTGTGACTGTGCTGGAGA 598
OY 301 ggcctgagaatgcttgggtgctgtgagatgagttccgtgtgtgtgtgtgtgtgt 359
    |||||||
DB 599 GGCCTGAGATCTCTGGGCTGCTGTGAGAGTGAAGTCTTGTGTGTGTGCTGCTGTGTG 658
OY 360 gtggcggagatgaacacacctgcgagga-gaacggcatgtgtatgcgacacacagccggg 418
    |||||||
DB 659 GTGGCGGAGATGAACACCTGTGAGGACAAAGCGCATGTGATGCGACATCAAGCGGG 718
OY 419 gaaca 423
    |||||
DB 719 GAACA 723

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RESULT 14
 BF794968 790 bp mRNA linear EST 12-JAN-2001
 LOCUS BF794968
 DEFINITION 60225867F1 NIH_MGC_85 Homo sapiens CDNA clone IMAGE:4339984 5',
 mRNA sequence.
 ACCESSION BF794968
 VERSION BF794968.1 GI:12100022

KEYWORDS

EST.
 human.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria;
 1 (bases 1 to 790)
 NIH-MGC <http://mgs.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Louis Staudt, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM951 row: f column: 17
 High quality sequence stop: 667.

FEATURES

Location/Qualifiers
 1. 790

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4339984"
 /clone_1ib="NIH_MGC-85"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lymph. Vector: pCMV-SPORT6. Site: 1: NotI;
 Site: 2: SalI; Cloned unidirectionally; oligo-dt primed.
 Average insert size 1.867 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC library."

BASE COUNT

178 a 216 c 263 g 133 t

ORIGIN

Query Match 17.8%; Score 382.6; DB 10; Length 790;
 Best Local Similarity 93.2%; Pred. No. 6.3e-70;
 Matches 422; Conservative 0; Mismatches 29; Indels 2; Gaps 2;

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OY 1 agatgagagacagacgaattactctgtgacacagatgactgtgagcagggagca 60
    |||||||
DB 312 AGATGAGAGACACAGCAATTAACCTGTGCACACAGATGACCTGTGGGAGGGGCA 371
OY 61 ctgccagtggtacaagagccgcaacaagaatccgagagagctgtgtgtgaagctc 120
    |||||||
DB 372 CTGCCAGTGTGTCAAGGCCGCCGACACAGAAATCCGAGAGCTGTGTGTGAAGTCT 431
OY 121 tcaaacctaccagctactctgcgcccgcgaggtgcaaggttgaagctctgc 180
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DB 432 TCACACTACACAGCTACCTGCGGCCCCGAGAGTGAAGTGAAGTGTGAGTCTGC 491
OY 181 ggaagctgagacacacgaacatcgtcaagctcttgcggtgagagagcgggagagc-c 239
    |||||||
DB 492 GGAAGCTGAAACCAACGAAATCCTGTAAGTCTTGTGCGTGAAGAGAGAGCGGACCC 551
OY 240 cggcagaaggtactgtgtagtactctccagtgagagcctgtgaaggtgtgtgag 299
    |||||||
DB 552 CGGACAGAGGTACTGTGATGAGTACTGCTCAATGGAGAGCTGCTGATGTGTGAG 611
OY 300 agccctgagaatgcttgggtgctgtgagatgagttccgtgtgtgtgtgtgtgtgt 359
    |||||||
DB 612 AGCCTGAGATGCTCTTGGGCTG-CTGAGGATGAGTCCCTGTGTGTGTGCTGTGTG 670
OY 360 gtggcggagatgaacacacctgcgaggaagcagcatgtgtatgcgacataacagcggg 419
    |||||||
DB 671 GTGGCGGAGATGAACACCTGTGAGGACAAAGCGCTGTGATGCGAATCAACCGGG 730
OY 420 aacatcatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 452
    |||||
DB 731 GGCCTCATGTGGCTCCAGGAAGAGGGGACAG 763

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 14, 2002, 19:06:08 ; Search time 103.46 Seconds
(without alignments)
768.692 Million cell updates/sec

Title: US-09-582-397A-2

Perfect score: 3674
Sequence: 1 MOSTANYLWHTDLDLGQAT.....LIDNNRIIRLNRPAPDPV 716

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3674	100.0	716	21	AAV93676 Amino acid sequenc
2	3674	100.0	716	21	AAAB01979 Human I-kappa-B k1
3	3670	99.9	716	21	AAV93683 Amino acid sequenc
4	3668	99.8	716	21	AAV93679 Amino acid sequenc
5	3668	99.8	716	21	AAV93680 Amino acid sequenc
6	3666	99.8	716	21	AAV93682 Amino acid sequenc
7	3665	99.8	716	21	AAV93681 Amino acid sequenc
8	3108.5	84.6	717	21	AAV80279 Murine I kappa B k
9	3102.5	84.4	717	21	AAAB01980 Murine I-kappa-B k
10	1719.5	46.8	729	19	AAAB0724 Human TR2 protein
11	1719.5	46.8	729	20	AAW79273 Human TR2 (TRAF2-a

12	1719.5	46.8	729	21	AAV44240
13	1719.5	46.8	729	22	AAE07905
14	1719.5	46.8	729	22	AAAB5601
15	1710.5	44.6	729	21	AAAB0280
16	1641	44.7	324	21	AAAB29859
17	1169	31.8	711	22	ABBS9265
18	705	19.2	254	22	AAAT2563
19	610	16.6	129	22	AAU17258
20	489	13.3	1214	21	AAV79152
21	472	12.8	148	22	AAU17243
22	424	11.5	756	19	AAW49097
23	424	11.5	756	19	AAW56328
24	424	11.5	756	20	AAV43247
25	424	11.5	756	20	AAV24051
26	424	11.5	756	20	AAV14515
27	424	11.5	756	20	AAW96158
28	424	11.5	756	20	AAW82499
29	424	11.5	756	20	AAW86163
30	424	11.5	756	20	AAW81563
31	424	11.5	1005	21	AAW81566
32	424	11.5	1007	21	AAW84882
33	424	11.5	1007	21	AAW84880
34	418	11.4	799	21	AAV79153
35	394.5	10.7	996	19	AAW85033
36	394	10.7	745	19	AAW56329
37	394	10.7	745	20	AAW82498
38	394	10.7	745	20	AAW81562
39	394	10.7	745	20	AAW81565
40	391	10.6	745	20	AAV24052
41	391	10.6	745	20	AAV14516
42	391	10.6	745	20	AAW96157
43	391	10.6	745	20	AAW86164
44	391	10.6	745	22	AAW67437
45	391	10.6	745	22	AAW67437

ALIGNMENTS

RESULT 1
ID: AAV93676
AAV93676 standard; Protein: 716 AA.
AC: AAV93676;
DT: 03-OCT-2000 (first entry)
XX: Amino acid sequence of a human IKK3 kinase.
XX: Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.
XX: Homo sapiens.
XX: WO200039308-A1.
XX: 06-JUL-2000.
XX: 24-DEC-1999; 99WO-JP07286.
XX: 24-DEC-1998; 98GB-0028704.
XX: (GLAX) GLAXO WELLCOME KK.
XX: Takemoto Y, Sakai Y, Hashimoto Y;
XX: WPI: 2000-475700/41.
XX: DR: N-PSDB: AAA47001.
XX: New IKK3 kinase protein and nucleotides encoding it, useful for
XX: screening for IKK3 protein modulators for treating inflammation, e.g.
XX: arthritis, atopic dermatitis or systemic lupus erythematosus
XX: Disclosure: Fig 4; 102pp; English.

XX The present sequence represents a human IKK3 kinase protein. The protein
 CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
 CC useful for screening for agents with anti-inflammatory activity.
 CC Compounds which exhibit IKK3 kinase modulating activity may be used
 CC in formulating a treatment or prophylaxis of a disorder responsive to
 CC the modulation of IKK3 kinase activity in a mammal. The proteins,
 CC their variants or fragments, derivatives, analogues or cells expressing
 CC them can also be used as immunogens to produce antibodies against IKK3
 CC protein, which may further be used to locate the protein in tissues
 CC expressing that protein.

CC Sequence 716 AA:

Query Match 100.0%; Score 3674; DB 21; Length 716;
 Best Local Similarity 100.0%; Pred. No. 1,4e-301;
 Matches 716; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOSTANLYMHTDLDLGGATASVYKARKKSGELVAVKVENTSYLRPREVQREPEVLR 60
 DB 1 mgsstanylwhtdllggatasyvykarnksgelvaavkventsylypreqvrefevlr 60
 QY 61 KLNHONIVKLEAVEETGSSROKVLVMEYCSGSLSTVLESPENAFGLPEDEFVLVRCVY 120
 DB 61 klnhoniavkaveelsgsrqkvlvmeycssgslstvlspenafiglpedefvlvrcv 120
 QY 121 AGNNHLRENGIVHRDIKPGNIMRLVGEQGSYKLTDFGARELDDDEKFEVSYGTEEYL 180
 DB 121 agnnhlrenglvhrdipgnimrlvgeegsyikltdfgareldddekfeyvsgteeyl 180
 QY 181 HPDMYERAVLRKPOOKAFGYTVDLMSIGVTLVYHAATGSLPFGGPRRKEIMYRTTTE 240
 DB 181 hpdmyeravlrkppokafgytvdlwslgvtylvhaatgslpfiggprmrkemyrttte 240
 QY 241 KPAGAIAGQRENGPLWSTYLPITCOLSLGLOSOLVPLIANTILEYQAKCWFQDFFA 300
 DB 241 kpagaiaqagrenplwstlylptcolslglosqlvplianllevegqkwcfdqffa 300
 QY 301 ETSDIQIQRVVVHVPSLSQAVLHNTIYIHAHNTIAIPEAVHAKOTSVAARHGEYLFEGHLCV 360
 DB 301 etsdliqrvvvhwpslsqavlhnyihahntiaifgeavhkgtsvaprhgeylfeghlc 360
 QY 361 LEPSVSOHNTAHTTASSPLTFSATPKGLAFDPALDVKEFPKYDLOADYNTAKGVYG 420
 DB 361 lepsvsohntahttasspltfstapkglafrdpaldvkefpykylodadynakgvyg 420
 QY 421 AGYQATLALRALDGOELMFRGLHMVEYQATCRRTLEAVRTSLYLSSTGTERFSSV 480
 DB 421 agyqatlalralldgoelmfrglhmvevqatcrrtleavrtsllylssstgterfssv 480
 QY 481 AGPEIDELKAAAELENSRLFTLAEVLSSQSNITTEQESLISNRELIVSRDOVHEDRST 540
 DB 481 agpeidelkaaaelelsrftlaevlsscsqnitteqeslissnrelivsrdivhedral 540
 QY 541 QOTGCCDKNFTYKOFKSRMRPGGYNEDQHKDKVNFSLAKRLIQVFOEECVQYK 600
 DB 541 qotgccdknftlykofksrmrpggynedqhkdkvnfslakrllqvfoeevqyk 600
 QY 601 QASLTVHGKMRVYVHETRNHLRLVGSVAACNTEAGOVESLSKLEELSHOLDORAG 660
 DB 601 qaslthgkrmrvyvhetrnhrlrlvgsvaacnteagovessklleelsholdorag 660
 QY 661 AQAAPPRIAPYPSPTRRKDLLHMOELCEGMKLLASDLNLRILNRPVAPPDV 716
 DB 661 aqasppriapypsptrrkdllhmoelcegmkllassdlldnrilnrpvpappdv 716

RESULT 2

ID AAB01979 standard; Protein; 716 AA.

XX AAB01979;
 AC AAB01979;

XX 25-SEP-2000 (first entry)

DT Human I-kappa-B kinase (IKK-1).

DE I-kappa-B kinase; IKK-1; human; serine/threonine kinase; NF-kappa-B;

KW nuclear factor kappa-B; inflammation; immune disorder; TRAF molecule;

XX I-TRAF related disorder; antinflammatory; immunostimulatory.

OS Homo sapiens.

XX WO200024908-A1.

XX 04-MAY-2000.

XX 26-OCT-1999; 99WO-JP05916.

XX 26-OCT-1998; 98JP-0304085.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Akira S, Shimada T;

XX WPI; 2000-350748/30.

XX N-PSDB; AAA52448.

XX Novel I-kappa-B kinase, IKK-1, capable of activating transcription

PT factor NF-kappa-B to inhibit expression of gene relating to immune

PT response, useful in drug compositions to treat inflammation and improve

PT immune response mechanism

PS Claim 1; Fig 3; 52pp; Japanese.

XX This sequence represents human I-kappa-B kinase (IKK-1). IKK-1 is

CC a serine/threonine kinase which can activate the transcription

CC factor NF-kappa-B (nuclear factor kappa-B). The invention relates

CC to the human and murine IKK-1 proteins (AAB01979, AAB01980), variants

CC thereof, and to nucleic acids encoding human and murine IKK-1 (AAA52448,

CC AAA52449). IKK-1 proteins are useful in drug compositions to treat

CC inflammation and improve the immune response mechanism. They may also be

CC used in preventing and treating diseases associated with the I-TRAF or

CC TRAF molecule.

XX Sequence 716 AA:

Query Match 100.0%; Score 3674; DB 21; Length 716;
 Best Local Similarity 100.0%; Pred. No. 1,4e-301;
 Matches 716; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOSTANLYMHTDLDLGGATASVYKARKKSGELVAVKVENTSYLRPREVQREPEVLR 60
 DB 1 mgsstanylwhtdllggatasyvykarnksgelvaavkventsylypreqvrefevlr 60
 QY 61 KLNHONIVKLEAVEETGSSROKVLVMEYCSGSLSTVLESPENAFGLPEDEFVLVRCVY 120
 DB 61 klnhoniavkaveelsgsrqkvlvmeycssgslstvlspenafiglpedefvlvrcv 120
 QY 121 AGNNHLRENGIVHRDIKPGNIMRLVGEQGSYKLTDFGARELDDDEKFEVSYGTEEYL 180
 DB 121 agnnhlrenglvhrdipgnimrlvgeegsyikltdfgareldddekfeyvsgteeyl 180
 QY 181 HPDMYERAVLRKPOOKAFGYTVDLMSIGVTLVYHAATGSLPFGGPRRKEIMYRTTTE 240
 DB 181 hpdmyeravlrkppokafgytvdlwslgvtylvhaatgslpfiggprmrkemyrttte 240
 QY 241 KPAGAIAGQRENGPLWSTYLPITCOLSLGLOSOLVPLIANTILEYQAKCWFQDFFA 300
 DB 241 kpagaiaqagrenplwstlylptcolslglosqlvplianllevegqkwcfdqffa 300
 QY 301 ETSDIQIQRVVVHVPSLSQAVLHNTIYIHAHNTIAIPEAVHAKOTSVAARHGEYLFEGHLCV 360
 DB 301 etsdliqrvvvhwpslsqavlhnyihahntiaifgeavhkgtsvaprhgeylfeghlc 360

QY 361 LEPVSAGHIAHTTASPLTLESTAI PKGLAFRDPALDPKFPVKVDLQADYNFAKGVLG 420
 DB 361 LEPVSAGHIAHTTASPLTLESTAI PKGLAFRDPALDPKFPVKVDLQADYNFAKGVLG 420
 QY 421 AGYQALRLARALLDGOELMFGLHVMVEVLQATCRRLLEVARTSLIYSSSLGTERESSV 480
 DB 421 AGYQALRLARALLDGOELMFGLHVMVEVLQATCRRLLEVARTSLIYSSSLGTERESSV 480
 QY 481 ACTPEIOELKAAELRSRLRLAEVLASRCSONITETQESLSLRELKSRDOVEDRSI 540
 DB 481 ACTPEIOELKAAELRSRLRLAEVLASRCSONITETQESLSLRELKSRDOVEDRSI 540
 QY 541 QOIOCCLDKMNFIYKQFKSRMRPGLGYNEEOIHKLDVNFSLHAKRLLOVFOECVQKY 600
 DB 541 QOIOCCLDKMNFIYKQFKSRMRPGLGYNEEOIHKLDVNFSLHAKRLLOVFOECVQKY 600
 QY 601 QASLVTGKRMVHETRNHLRLVGCVAACNTAAGVQESLSKLELSHOLLDRAGK 660
 DB 601 QASLVTGKRMVHETRNHLRLVGCVAACNTAAGVQESLSKLELSHOLLDRAGK 660
 QY 661 AGASPPPIAPYSPTRKDLLHMOELCEGKMLASDLLDNNRIERLNRPAPPDV 716
 DB 661 AGASPPPIAPYSPTRKDLLHMOELCEGKMLASDLLDNNRIERLNRPAPPDV 716

RESULT 3

AAV93683
 ID AAV93683 standard; Protein; 716 AA.

AAV93683;
 DT 03-OCT-2000 (first entry)

DE Amino acid sequence of a human IKK3 kinase mutant protein.

KW Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.

OS Synthetic.

OS Homo sapiens.

PN WO200039308-A1.

PD 06-JUL-2000.

PF 24-DEC-1999; 99WO-JP07286.

PR 24-DEC-1998; 98GB-0028704.

PA (GLAX) GLAXO WELLCOME KK.

PI Takemoto Y, Sakai Y, Hashimoto Y;

DR WPI: 2000-475700/41.

PT New IKK3 kinase protein and nucleotides encoding it, useful for
 screening for IKK3 protein modulators for treating inflammation, e.g.
 arthritis, atopic dermatitis or systemic lupus erythematosus
 PS Disclosure; Page 94-97; 102pp; English.

XX AAV93679-83 represent human IKK3 kinase mutant proteins. The IKK3 kinase
 CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
 CC useful for screening for agents with anti-inflammatory activity.
 CC Compounds which exhibit IKK3 kinase modulating activity may be used
 CC in formulating a treatment or prophylaxis of a disorder responsive to
 CC the modulation of IKK3 kinase activity in a mammal. The proteins,
 CC their variants or fragments, derivatives, analogues or cells expressing
 CC them can also be used as immunogens to produce antibodies against IKK3
 CC protein, which may further be used to locate the protein in tissues
 CC expressing that protein.
 XX Sequence 716 AA.

Query Match 99.9%; Score 3670; DB 21; Length 716;
 Best Local Similarity 99.9%; Pred. No. 3.1e-301;
 Matches 715; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOSTANLMTHTDILLGAGATASVYKARNKSGELVAVKVENTSYLAPREVQREFEYL 60
 DB 1 mstanlylwhtddillggatasyvkaroksgelvaavvfnctsyilpreqvrefeaylr 60
 QY 61 KLNQNLVYKLFVAVETGSSROKVLVMEYSSGSLSVLESEPMFGLPEDEFVVLRCV 120
 DB 61 klnqnlyvklfaveetgssrkvlvmeyscgslsvlesepmafglpedefvvlrcv 120
 QY 121 AGMNLRENGIVHRDIKGNITMRVLVEGQSIYKLTDFGARELDDEKFEVSYGTEYL 180
 DB 121 agmnhlrengivhrdikhgnitmrvlveggsglykltfdgaareldeekfevysygeyl 180
 QY 181 HPDMTERAVLRKPOOKAFGVTVDLMSIGVTLVHAATGSLPFIPIGGRRKKEIMRTYTE 240
 DB 181 hpdmteravlrkpgqkafgvtevdmsigvtlvhaatgslpfiipiggrkneimrylte 240
 QY 241 KPAGIAGQRRNGPLRMSYTLPTCOLSIGLSQSLVPLANTILEYQAKCMGPDQFPA 300
 DB 241 kpagialagqrrngplrmsytlptcolsiglsqslvplantilevqakcmgpdqfpa 300
 QY 301 ETSDLIQRVNVHVESLSQAVLHNTIYTHAHTIATFOEAVHRKQTSVAPRHQYLFEGHLCV 360
 DB 301 etsdliqrvvvhvveslsqavlhntiythahntiatfoevhvkqtsvaprhqylfeghlc 360
 QY 361 LEPVSAGHIAHTTASPLTLESTAI PKGLAFRDPALDPKFPVKVDLQADYNFAKGVLG 420
 DB 361 LEPVSAGHIAHTTASPLTLESTAI PKGLAFRDPALDPKFPVKVDLQADYNFAKGVLG 420
 QY 421 AGYQALRLARALLDGOELMFGLHVMVEVLQATCRRLLEVARTSLIYSSSLGTERESSV 480
 DB 421 AGYQALRLARALLDGOELMFGLHVMVEVLQATCRRLLEVARTSLIYSSSLGTERESSV 480
 QY 481 ACTPEIOELKAAELRSRLRLAEVLASRCSONITETQESLSLRELKSRDOVEDRSI 540
 DB 481 ACTPEIOELKAAELRSRLRLAEVLASRCSONITETQESLSLRELKSRDOVEDRSI 540
 QY 541 QOIOCCLDKMNFIYKQFKSRMRPGLGYNEEOIHKLDVNFSLHAKRLLOVFOECVQKY 600
 DB 541 QOIOCCLDKMNFIYKQFKSRMRPGLGYNEEOIHKLDVNFSLHAKRLLOVFOECVQKY 600
 QY 601 QASLVTGKRMVHETRNHLRLVGCVAACNTAAGVQESLSKLELSHOLLDRAGK 660
 DB 601 QASLVTGKRMVHETRNHLRLVGCVAACNTAAGVQESLSKLELSHOLLDRAGK 660
 QY 661 AGASPPPIAPYSPTRKDLLHMOELCEGKMLASDLLDNNRIERLNRPAPPDV 716
 DB 661 AGASPPPIAPYSPTRKDLLHMOELCEGKMLASDLLDNNRIERLNRPAPPDV 716

RESULT 4

AAV93679
 ID AAV93679 standard; Protein; 716 AA.

AAV93679;
 DT 03-OCT-2000 (first entry)

DE Amino acid sequence of a human IKK3 kinase mutant protein.

KW Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.

OS Synthetic.

OS Homo sapiens.

PN WO200039308-A1.

PD 06-JUL-2000.

XX 24-DEC-1999; 99WO-JP07286.
 XX 24-DEC-1998; 98GB-0028704.
 XX (GLAX) GLAXO WELLCOME KK.
 XX Takemoto Y, Sakai Y, Hashimoto Y;
 XX WPI; 2000-475700/41.
 XX
 XX New IKK3 kinase protein and nucleotides encoding it, useful for
 XX screening for IKK3 protein modulators for treating inflammation, e.g.
 XX arthritis, atopic dermatitis or systemic lupus erythematosus -
 XX
 XX Disclosure; Page 79-82; 102pp; English.
 XX
 XX AAY93679-83 represent human IKK3 kinase mutant proteins. The IKK3 kinase
 XX is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
 XX useful for screening for agents with anti-inflammatory activity.
 XX Compounds which exhibit IKK3 kinase modulating activity may be used
 XX in formulating a treatment or prophylaxis of a disorder responsive to
 XX the modulation of IKK3 kinase activity in a mammal. The proteins,
 XX their variants or fragments, derivatives, analogues or cells expressing
 XX them can also be used as immunogens to produce antibodies against IKK3
 XX protein, which may further be used to locate the protein in tissues
 XX expressing that protein.
 XX
 XX Sequence 716 AA;
 SQ

Query Match 99.8%; Score 3668; DB 21; Length 716;
 Best Local Similarity 99.9%; Pred. No. 4.5e-301;

Matches 715; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOSTANYLMDHDDLLGOGATASVYKARKKSGELVAVKFNFTSYLPRREVQREPEVLR 60
 DB 1 mgtstanylwhdtdllggatatsvykarkksgelvavkfnftsyilpreqvarefevir 60
 QY 61 KLNHONIVKLEFAVEETGSSROKVLVMEYCSSGSLVLESPENAFGLPEDDEFVLVRCV 120
 DB 61 klnhoniivklfaveetgssrkvlymeycssgslvlespenafglpedefvlvrcv 120
 QY 121 AGMNHLENGIVHNDIKPGNIMRLVGEESGSIYKLTDFGARELDDDEKVSYGTEEYL 180
 DB 121 agmnhleengivhndikpgnimrlvgeegslykltdfgaareldddekvtvygteeyl 180
 QY 181 HPDMYERAVLRKPOQKAFGYTVLWLSIGVLYLHAATGSLPFIFGGRPRRKKEIMYRTTTE 240
 DB 181 hpdmyeravlrkpoqkafgytvdlwlsigvlylhaatgsplfifggrprnrkkelmyrttte 240
 QY 241 KPGATAGAGRRRNGRPLEMSYTPITCQLSLGIQSLVPLANTILEVEQAKCWGPDQFPA 300
 DB 241 kpgatagagrrngrplemsytpitcqlslgiqslvplantilleveqakcwgpdqfpa 300
 QY 301 ETSDDIQRVVVHVFSLSQAVLHHIYIHAHNTIAIPEAVHAKOTSVAPRHOEYLFEGHLCV 360
 DB 301 etsddiqrvvvhvfslsqavllhlyihahntiaifgaavhkgtsvprhoylfeghlc 360
 QY 361 LEPSVSNQIHARTTASSPLTLESTAIIPKGLAFDPALDVPKVPKVDLOADYNTAKVLG 420
 DB 361 lepsvsnqhahrttasspltlestaiipkglafdpaldvpkfvpkvdldadynytakvg 420
 QY 421 AGYQALRLARLALDGOELMFRGLHWMVEVLAQTCRRTLEVARSLIYSSSLGTERFSSV 480
 DB 421 agyqalrlaralldgoelmfrglhwmvevlaqtcrrtlevarslilyssslgterfssv 480
 QY 481 AGTPEIQELKAAAEELSRRLTAELVSRCSQNTTFOESTSLNRLFLVSRDOVHEDRSI 540
 DB 481 agtpeiqelkaaeelsrrltaelvsrcsqntetqeslslnrlflvsvrdovhedrsi 540
 QY 541 QOIQCCLDKMNFTYKOPFKSRMRPGGYNEQDILKLDKVFNSHLAKRLQVFOEECVQKY 600
 DB 541 qoioqccldkmnftykopfkssrmpggyneqdihkldkvnfshlakrlqvfoeevcyky 600

DB 541 qdqqccldkmnftlykqfkksrmzpglyneeqdihkldkvnfshlakrlqvfeecvqky 600
 QY 601 QASLVTHGKRMRYVHETRNHLRVGCSVAACNTAOGVDSLSKLEELSHQLDDRAKG 660
 DB 601 qaslvthgkrmyvhetrnhlrvlgcsvaacntaogvdslskleelshqlddraqk 660
 QY 661 AQASPPPIAPYPSPTRRDILLHMOELCEGKMLIASDLDNNPIRELNVPVAPPV 716
 DB 661 agaspppiapypsptrrdkillhmoelcegmklliasdldnnrierlnvpappv 716

RESULT 5

AAY93680
 ID AAY93680 standard; Protein; 716 AA.

XX AAY93680;

AC 03-OCT-2000 (first entry)

DE Amino acid sequence of a human IKK3 kinase mutant protein.

XX Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.

OS Synthetic.

XX Homo sapiens.

PN WO200039308-A1.

PD 06-JUL-2000.

XX 24-DEC-1999; 99WO-JP07286.

XX 24-DEC-1998; 98GB-0028704.

XX (GLAX) GLAXO WELLCOME KK.

XX Takemoto Y, Sakai Y, Hashimoto Y;

XX WPI; 2000-475700/41.

XX New IKK3 kinase protein and nucleotides encoding it, useful for

XX screening for IKK3 protein modulators for treating inflammation, e.g.

XX arthritis, atopic dermatitis or systemic lupus erythematosus -

XX Disclosure; Page 82-86; 102pp; English.

XX AAY93679-83 represent human IKK3 kinase mutant proteins. The IKK3 kinase

XX is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is

XX useful for screening for agents with anti-inflammatory activity.

XX Compounds which exhibit IKK3 kinase modulating activity may be used

XX in formulating a treatment or prophylaxis of a disorder responsive to

XX the modulation of IKK3 kinase activity in a mammal. The proteins,

XX their variants or fragments, derivatives, analogues or cells expressing

XX them can also be used as immunogens to produce antibodies against IKK3

XX protein, which may further be used to locate the protein in tissues

XX expressing that protein.

XX Sequence 716 AA;

SQ

Query Match 99.8%; Score 3668; DB 21; Length 716;
 Best Local Similarity 99.7%; Pred. No. 4.5e-301;
 Matches 714; Conservative 2; Mismatches 0; Indels 0; Gaps 0;


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|||||
Db 121 agmnhlrenglvhrdtkpgnlmrlvgeegqslyklldfgaaeldddekfvsygleyl 180
OY 181 HSDMYERAVLRKPOOKAEVTVDLMSIGVTLYHAATGSLPFIPEGGRNKKIMYRITTE 240
Db 181 hsdmyeravlrkpgkafgvtvdlwslvlyhaatgslpfipeggrnkkimyrilte 240
OY 241 KPAGAIAGAQRENGPBLEMSYTLPTTCQLSLGSLQSLVPLIANILEVEQAKCWGDQFPA 300
Db 241 kpagaiaagqrrengpblemsytlpttcqlslgslqslvplianillevegakcwgdqffa 300
OY 301 EFSDLIQRVVHVFSLSQAVLHHIYTHAHTAIROEAVHKOTSVAPRHOEYLFEGHLCV 360
Db 301 efsdlilqrvvhvffslsqavlnhiythahntaifgeavhkvtsvaprhqeylfeghlc 360
OY 361 LEPSVSAQHIAHTTASSPLTFLSTAIKGLAFRDPALDVPKVPVVDLOADNTAKGVLG 420
Db 361 lepsvsaqhiahntasspltlfstalpkglaftrdpaldvpkvpvvdloadyntakgylg 420
OY 421 AGYQALRLARALLDGOELMFRGLHWMVEVLOATCRRTLEVARTSLYLSSSLGTERFSSV 480
Db 421 agyqalrlaralldgqelmfgrlhwmevlgatcrrtleavrtsllylssslgterfssv 480
OY 481 AGTPEIQELKAAELRSRLRTLAELVSRCSQNTTFOESLSLNRELVSROQVHEHDSI 540
Db 481 agtpeiqelkaaelrsrlrtlaevlsrscqnltelqeslslnrelvksrdqvhdetsi 540
OY 541 QOIQCCLDMNFYIKQFKSRMPGLGYNEQIHKLDKNFSLAKRLLOVQEBGVOKY 600
Db 541 qoiqccldmnfyikqfkksrmpglgynqei hkdvnfshlarkrlloqvqebcvqky 600
OY 601 QASLVTHGKRMVYHETRNHLRLVGCSSVAACNTAEQVQESLSKLELSHOLLDRAGK 660
Db 601 qaslvthgkrmvhethrnlrlvgcvsaaenteagvqeslskilleeshqllqdrakg 660
OY 661 AQAAPPPIAPYSPPTRKDLLHMQELCEGKMLASDLDDNNRIETELNRPAPPDV 716
Db 661 aqaspppiapyspptrkdlldmqelcegmkllaasdlldnnrietelnrvpappdv 716

RESULT 6
AA93682
ID AA93682 standard; Protein: 716 AA.
XX
AC AA93682;
XX
DT 03-OCT-2000 (first entry)
XX
DE Amino acid sequence of a human IKK3 kinase mutant protein.
XX
KW Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN WO200039308-A1.
XX
PD 06-JUL-2000.
XX
PF 24-DEC-1999; 99WO-JP07286.
XX
PR 24-DEC-1998; 98GB-0028704.
XX
PA (GLAX) GLAXO WELLCOME KK.
XX
PI Takemoto Y, Sakai Y, Hashimoto Y;
XX
DR WPI; 2000-475700/41.
XX
New IKK3 kinase protein and nucleotides encoding it, useful for
PT screening for IKK3 protein modulators for treating inflammation, e.g.
PT arthritis, atopic dermatitis or systemic lupus erythematosus
XX

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PS Disclosure: Page 90-93; 102pp; English.
XX
CC AA93679-83 represent human IKK3 kinase mutant proteins. The IKK3 kinase
CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
CC useful for screening for agents with anti-inflammatory activity.
CC Compounds which exhibit IKK3 kinase modulating activity may be used
CC in formulating a treatment or prophylaxis of a disorder responsive to
CC the modulation of IKK3 kinase activity in a mammal. The proteins,
CC their variants or fragments, derivatives, analogues or cells expressing
CC them can also be used as immunogens to produce antibodies against IKK3
CC protein, which may further be used to locate the protein in tissues
CC expressing that protein.
XX
SQ Sequence 716 AA;

Query Match 99.8%; Score 3666; DB 21; Length 716;
Best Local Similarity 99.7%; Pred. No. 6.7e-301;
Matches 714; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MOSTANYLMTDLDLGOCATASVYKARKKSGELVAVFNTSYLRPREVOVREFEVLR 60
Db 1 mgsstanylhtddllggatasyvkarinksgelavavfntsylyrprevyrefeylr 60
OY 61 KLNHONIVKLEAVEETGSRQKVLVMEYCSGSLSLVLESPENAFGLPEDEFJVLKCV 120
Db 61 klnhoni vkleaveetgsrqlvmeyscsgslslvleepenafglpedeflvlrvcv 120
OY 121 AGMNLHRENGIYHRDITKPNIMRLVGEQOSTYKLTIDGCAAELEDDDKFVSYTEEYL 180
Db 121 agmnhlrenglvhrdtkpgnlmrlvgeegqslyklldfgaaeldddekfvsygleyl 180
OY 181 HSDMYERAVLRKPOOKAEVTVDLMSIGVTLYHAATGSLPFIPEGGRNKKIMYRITTE 240
Db 181 hsdmyeravlrkpgkafgvtvdlwslvlyhaatgslpfipeggrnkkimyrilte 240
OY 241 KPAGAIAGAQRENGPBLEMSYTLPTTCQLSLGSLQSLVPLIANILEVEQAKCWGDQFPA 300
Db 241 kpagaiaagqrrengpblemsytlpttcqlslgslqslvplianillevegakcwgdqffa 300
OY 301 EFSDLIQRVVHVFSLSQAVLHHIYTHAHTAIROEAVHKOTSVAPRHOEYLFEGHLCV 360
Db 301 efsdlilqrvvhvffslsqavlnhiythahntaifgeavhkvtsvaprhqeylfeghlc 360
OY 361 LEPSVSAQHIAHTTASSPLTFLSTAIKGLAFRDPALDVPKVPVVDLOADNTAKGVLG 420
Db 361 lepsvsaqhiahntasspltlfstalpkglaftrdpaldvpkvpvvdloadyntakgylg 420
OY 421 AGYQALRLARALLDGOELMFRGLHWMVEVLOATCRRTLEVARTSLYLSSSLGTERFSSV 480
Db 421 agyqalrlaralldgqelmfgrlhwmevlgatcrrtleavrtsllylssslgterfssv 480
OY 481 AGTPEIQELKAAELRSRLRTLAELVSRCSQNTTFOESLSLNRELVSROQVHEHDSI 540
Db 481 agtpeiqelkaaelrsrlrtlaevlsrscqnltelqeslslnrelvksrdqvhdetsi 540
OY 541 QOIQCCLDMNFYIKQFKSRMPGLGYNEQIHKLDKNFSLAKRLLOVQEBGVOKY 600
Db 541 qoiqccldmnfyikqfkksrmpglgynqei hkdvnfshlarkrlloqvqebcvqky 600
OY 601 QASLVTHGKRMVYHETRNHLRLVGCSSVAACNTAEQVQESLSKLELSHOLLDRAGK 660
Db 601 qaslvthgkrmvhethrnlrlvgcvsaaenteagvqeslskilleeshqllqdrakg 660
OY 661 AQAAPPPIAPYSPPTRKDLLHMQELCEGKMLASDLDDNNRIETELNRPAPPDV 716
Db 661 aqaspppiapyspptrkdlldmqelcegmkllaasdlldnnrietelnrvpappdv 716

RESULT 7
AA93681
ID AA93681 standard; Protein: 716 AA.
XX

```

AC AAY93681;
 XX 03-OCT-2000 (first entry)
 XX Amino acid sequence of a human IKK3 kinase mutant protein.
 DE Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX W0200039308-A1.
 XX
 PD 06-JUL-2000.
 XX
 XX 24-DEC-1999; 99WO-JP07286.
 XX
 XX 24-DEC-1998; 98GB-0028704.
 XX
 PA (GLAX) GLAXO WELLCOME KK.
 XX
 XX Takemoto Y, Sakai Y, Hashimoto Y;
 XX WPI; 2000-475700/41.
 XX
 PT New IKK3 kinase protein and nucleotides encoding it, useful for
 PT screening for IKK3 protein modulators for treating inflammation, e.g.
 PT arthritis, atopic dermatitis or systemic lupus erythematosus
 XX
 XX Disclosure; Page 86-90; 102pp; English.
 XX
 CC AAY93679-83 represent human IKK3 kinase mutant proteins. The IKK3 kinase
 CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
 CC useful for screening for agents with anti-inflammatory activity.
 CC Compounds which exhibit IKK3 kinase modulating activity may be used
 CC in formulating a treatment or prophylaxis of a disorder responsive to
 CC the modulation of IKK3 kinase activity in a mammal. The proteins,
 CC their variants or fragments, derivatives, analogues or cells expressing
 CC them can also be used as immunogens to produce antibodies against IKK3
 CC protein, which may further be used to locate the protein in tissues
 CC expressing that protein.
 CC
 XX
 XX Sequence 716 AA:

Query Match 99.8%; Score 3665; DB 21; Length 716;
 Best Local Similarity 99.7%; Pred. No. 8.1e-301;
 Matches 714; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

YY 1 MOSTANYLWHTDLDLGGATASVYKANKKSGELVAVKVNNTSYLRPREVQYREFEVL 60
 DB 1 mgsctanylwhtddlggataasykankksgelvaavkvnttsylrprevyrefevlr 60
 YY 61 KLNHONIVKLFVAVETGSGRQKLVMEYCSGSLSVLESPENAFGLPEDEFLVLR 120
 DB 61 klhqnivklfaveetgsgskvlmeyesgslsvlepenafglpedeflvlr 120
 YY 121 AGNHNLRKNCIVHRDIKPGNIMRLVGEESGSIYKLPDFGAERLDDKRFVSVYGTET 180
 DB 121 agnhnlrncivhrdikpgnimrlvgeegsglyklldfgareldddakrfvaygtye 180
 YY 181 HPMYERAVLRKPOKAFGTVLMSIGVTLVHAATGSLPRTFFGGRPRRKEMLMTTTE 240
 DB 181 hpmyeravlrkpoakafgvtvlmsigvtlvhaatgslprrtffggrprrrkeltmttte 240
 YY 241 KPAAGIAGAGRRENGPLEWSTYLPITCOLSLGQSOLVPLIANILFEVQAKCGFQFPA 300
 DB 241 kpaaglagagrenplwstypitcolslgqsolvplianilleveqakcgfqafta 300
 YY 301 EFSDDIQRVWVHVSLSQAVLHHTYTHAHNTAIFQEAHVAKQTSVAPRRQETLFECHLCV 360
 DB 301 etfddilqrwvvhvslsqavlhhtylhahntaifqeahvkhqtsvaprrqeylfechlc 360

QY 361 LEPVSNAOHIAHTTASSPLTLFSTALPKGLAFDPDALDVPKFVPPKVDLOADYNFAKGV 420
 DB 361 lepsvaoghiahtasspltlfstalpkglafdpdalvdkfvpkvdloadyntakg 420
 QY 421 AGYQALRLRALLDGQELMFRGLHWVWEVLQATCRRTLEVARTSLYSSSITGERFSSV 480
 DB 421 agyqalrlralldgqelmfrglhwvwevlqatcrtrlevartsllyssstgerfssv 480
 QY 481 AGTPEIOLKAAAEKRSRLTAEVLSRCSQNTTEQESLSLNRELKVSROQVHDSI 540
 DB 481 agtpeiolkaaaelrsrltaevlsrscsqntteqeslslnrelkvsrqvhdssi 540
 QY 541 QOIQCCLDKKNFTYKQFKSRMRPGGLGYNEEOIHKDKVNFSLAKRLIQVGEQVQY 600
 DB 541 qoiqccldknftykqfkssrmpgglgyneeqihkdvnfslakrllyqvgecvqy 600
 QY 601 QASLVTHGKRMRVYHETRNHLRVGCSVAACNTAAGVQESLSKLELSHQLDRAKG 660
 DB 601 qaslvthgkrmrvyhetrnhlrvlgcsvaacntaagvqeslskllleishqlldrakg 660
 QY 661 AQASPPPIAPYSPPTKKDLLHMQELCEGMKILASLDLNNKILRLNRPAPPV 716
 DB 661 aqaspppiapyspplrkdllhmqelcegmklilaslldnnrlrlrtnrpapppv 716

RESULT 8
 AAY80279
 ID AAY80279 standard; Protein; 717 AA.
 XX
 AC AAY80279;
 XX
 DT 26-MAY-2000 (first entry)
 XX
 DE Murine I kappa B kinase-related kinase 1 SEQ ID NO:2.
 XX
 KW Mouse; murine; I kappa B kinase-related kinase; IKR-1; IKR-2;
 KW protein kinase; immunomodulatory; antiinflammatory; antimicrobial;
 KW cytosolic; autoimmune; inflammatory; infection; neoplastic disease.
 OS Mus sp.
 XX
 XX W0200008179-A1.
 XX
 PD 17-FEB-2000.
 XX
 PF 04-AUG-1999; 99WO-US17578.
 XX
 PR 04-AUG-1998; 98US-0095269.
 PR 11-SEP-1998; 98US-0099973.
 PR 05-FEB-1999; 99US-0118783.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Bird TA, Vitca GD;
 XX
 DR WPI; 2000-195583/17.
 DR N-35DB; AA295275.
 XX
 PT Novel kappa B-kinase related kinases IKR-1 and IKR-2 used as molecular
 PT weight markers and in peptide fragmentation studies
 XX
 PS Claim 13; Fig 3; 85pp; English.
 XX
 PS The present sequence represents murine I kappa B-kinase related kinase 1
 CC (IKR-1). IKR proteins have immunomodulatory, antiinflammatory,
 CC antimicrobial and cytosolic activities. IKR polynucleotides can be
 CC used to express the proteins, and as probes to identify nucleic acids
 CC encoding proteins having kinase activity. IKR-1 and IKR-2 proteins and
 CC fragmented polypeptides are used for purifying proteins, e.g. to purify
 CC binding partner proteins; to measure protein activity, e.g. as quality
 CC assurance agents to monitor shelf life and stability of binding partner
 CC proteins. They may also be used as research agents, e.g. in assays to
 CC determine protein kinase activity, to identify novel molecules involved

CC in signal transduction pathways, and to identify therapeutic compounds,
CC to identify substances which interfere with the rate of substrate
CC phosphorylation (such compounds would be useful for the treatment of
CC autoimmune, inflammatory, infectious or neoplastic diseases), as
CC molecular weight and isoelectric focusing markers, as controls for
CC peptide fragmentation, identification of unknown proteins, e.g. by
CC comparison with proteins in databases and for preparation of antibodies.
CC The antibodies can be used in assays to detect the presence of the
CC protein, and to purify the protein by immunofluorescence chromatography. The
CC antibodies can also be used to block binding of the IKK polypeptides to
CC their binding partners.

XX Sequence 717 AA:

Query Match 84.6%; Score 3108.5; DB 21; Length 717;
Best Local Similarity 82.9%; Pred. No. 9,1e-254;
Matches 598; Conservative 56; Mismatches 58; Indels 9; Gaps 4;

QY 1 MOSTANYLWHTDLDLGGATASVYKARNKSGELVAVKVFNTSYLRPREVOYREEVLR 60
DB 1 mgtctnylwhtdlldlggataasykarnksgvavavkfnsasyrripvqvylevlr 60
QY 61 KLNHONIVKLFVAVETGSGROKVLVMEYSSGSLVLESPEKARGLFDEFLVYLRCVY 120
DB 61 rlnhqnivklfaveetgsgrokvlvmeyscgslslsvledpentiqlseeflvylrcv 120
QY 121 AGNHLRENGIVHRDIPKGNIMRLVGEOSIYKLTDFGARELDDDEKFSVYGGEEYL 180
DB 121 agnmhlrengivhrdipkgnimrlvgeegslyklsdfgaarldddekfsvyggely 180
QY 181 HPDMYERAVLRKPKQKAFVTVDLMSIGVLYHAATGSLPFIPFGGPRNKEIMYRITTE 240
DB 181 hpdmyeravlrkpkqkafvtdvmsigvlyhaatgslpfpfggprnkeimyritle 240
QY 241 KPAGATAGAGORRENGPLEMSTYLPITCOLSLGQSOLVPIILANILEVQAKCGEFOFRA 300
DB 241 kpagaatagagorrengplemstypitcolslmgisqnlvpiilanilleveedkcgfddfa 300
QY 301 ETSDILORVVVHFSLSQAVLHHIYTHANTIAIPEAVHAKOTSVAIRHOEYLFEGHLCY 360
DB 301 etsdilgrtvhvfslpqrqlhvyhahntiaiflaevqgenvpdkqeylfeghpcv 360
QY 361 LEPVSASQHTAHTTASSPLTLESTA--IKGLAFRDPALDVPKFPKVDLQADYNTAKGY 418
DB 361 leplsasqhahhaaspltlfsmssdtpkqlaftrdpaldvpkfpkvdldqadystakgy 420
QY 419 LGAGYQALRLARALDGOELMFRGLHVMVEVLOATCRRTLEVARTSLVSSLSGTERFS 478
DB 421 lggagqlarlaraldgoelmfrglhvmvevloatcrrtlevartrslvsslsgerfs 480
QY 479 SVAGTEPDELKAAAEELSRRLTAEVLSRCSONITETQESLSLNRELKVSROVHEH- 537
DB 481 svagmpdvgerkeatetrtrlgtselsskshvteqtslsgellknrdqghedn 540
QY 538 RSTQLOQCCLDKNNFTYKQKSSRMRLGLOYNBQTHKLDKVPFSLAKLLQVPOGEVY 597
DB 541 kstqlqcccldknnfitykqkssrmrpglsyneeqlhldkvnfshakllayfgeev 600
QY 598 OKTQASLVTHGKRMVVEHETRNHLRLVGCSSVACNTPAOCVQESLSKLELSELHQLQDR 657
DB 601 qktqvslvtgkrmvvehetrnhllrvgcsvgacntpaocvqeslnklldf-----qllldr 656
QY 658 A--KGASPPPIAIVPSPTRKDLLHMOBELCEGMKLASDLDNNRILRLRVAPPD 715
DB 657 aasegaevsppmaipbpkdkdivfmgelcndmkllafdlqdnrlterlhvpsapd 716
QY 716 V 716
DB 717 V 717

RESULT 9

AAB01980
ID AAB01980 standard; Protein: 717 AA.

AC AAB01980;

DT 25-SEP-2000 (first entry)

DE Murine I-kappa-B kinase (IKK-1).

KW I-kappa-B kinase; IKK-1; murine; serine/threonine kinase; NF-kappa-B;
KW nuclear factor kappa-B; inflammation; immune disorder; TRAF molecule;
KW I-TRAF related disorder; antiinflammatory; immunostimulatory.

OS Mus sp.

PN W0200024908-A1.

PD 04-MAY-2000.

PF 26-OCT-1999; 99WO-JP05916.

PR 26-OCT-1998; 98JP-0304085.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PI Akira S, Shimada T;

DR WPI: 2000-350748/30.

XX N-PSDB: AAA52449.

PT Novel I-kappa-B kinase, IKK-1, capable of activating transcription
PT factor NF-kappa-B to inhibit expression of gene relating to immune
PT response, useful in drug compositions to treat inflammation and improve
PT immune response mechanism

PS Claim 1; Fig 3; 52pp; Japanese.

XX This sequence represents murine I-kappa-B kinase (IKK-1). IKK-1 is
XX a serine/threonine kinase which can activate the transcription
XX factor NF-kappa-B (nuclear factor kappa-B). The invention relates
XX to the human and murine IKK-1 proteins (AAB01979, AAB01980), variants
XX thereof, and to nucleic acids encoding human and murine IKK-1 (AAA52448,
XX AAA52449). IKK-1 proteins are useful in drug compositions to treat
XX inflammation and improve the immune response mechanism. They may also be
XX used in preventing and treating diseases associated with the I-TRAF or
XX TRAF molecule.

SO Sequence 717 AA:

Query Match 84.4%; Score 3102.5; DB 21; Length 717;
Best Local Similarity 82.7%; Pred. No. 2,9e-253;
Matches 596; Conservative 58; Mismatches 58; Indels 9; Gaps 4;

QY 1 MOSTANYLWHTDLDLGGATASVYKARNKSGELVAVKVFNTSYLRPREVOYREEVLR 60
DB 1 mgtctnylwhtdlldlggataasykarnksgvavavkfnsasyrripvqvylevlr 60
QY 61 KLNHONIVKLFVAVETGSGROKVLVMEYSSGSLVLESPEKARGLFDEFLVYLRCVY 120
DB 61 rlnhqnivklfaveetgsgrokvlvmeyscgslslsvledpentiqlseeflvylrcv 120
QY 121 AGNHLRENGIVHRDIPKGNIMRLVGEOSIYKLTDFGARELDDDEKFSVYGGEEYL 180
DB 121 agnmhlrengivhrdipkgnimrlvgeegslyklsdfgaarldddekfsvyggely 180
QY 181 HPDMYERAVLRKPKQKAFVTVDLMSIGVLYHAATGSLPFIPFGGPRNKEIMYRITTE 240
DB 181 hpdmyeravlrkpkqkafvtdvmsigvlyhaatgslpfpfggprnkeimyritle 240
QY 241 KPAGATAGAGORRENGPLEMSTYLPITCOLSLGQSOLVPIILANILEVQAKCGEFOFRA 300
DB 241 kpagaatagagorrengplemstypitcolslmgisqnlvpiilanilleveedkcgfddfa 300

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QY 301 ETSIDILQRVVHVFSLSQAVLHHIYIHAHNTAIFQEAHVHKTQSVAPRHOEYLFEGHLCV 360
Db 301 etsidilqrvvhvfvslsqavlhhiyihahntaifqeahvhktsvaprhoeylfeghlc 360
QY 361 LEPSVSAOHIAHTTASSPLTLPSTA--IPKGLAFRDPALDVPKFPVKYDLADYNTRAKGV 418
Db 361 lepsvsaohiahtasspltlpsta--ipkglafrdpaladvpkfvpkydoadyntrakgv 418
QY 419 LGAGQALRLARALLDQGLMEFGLHWMEVLAQTCRTELEVATSLIYSSSGTERFS 478
Db 419 lgagqalrlaralldqglmefglhwmevlaqtcrtelvatstliysssgterfs 478
QY 421 lgaqgqalwlarvllldqgalhrlhvwlevgldcqqclvtaltallygsslgterfs 480
Db 421 lgaqgqalwlarvllldqgalhrlhvwlevgldcqqclvtaltallygsslgterfs 480
QY 479 SVAGTPEIOELKAAAEKLSRLTAEVLSRCSQNTTQESLSINBELVSRDQVED- 537
Db 479 svagtpeioelkAAAEKLSRLTAEVLSRCSQNTTQESLSINBELVSRDQVED- 537
QY 538 RSIOOIOCCLDKMFYKQFKSRMRPGLGNEFOIHKDKVNFSLAKRLLOVFOECV 597
Db 541 ksqdkgicldkmfilykfkksrmrpglsyneqihkdkvnfshakrllgyfgecv 600
QY 598 OKYQASLTGKRRRVVHETRNHLRLVGCVAACNTGAGVOESLSKILEELSHQLQDR 657
Db 601 qtygvslthgkrmrvgqrgnqhllghsvatcnsearqageslnkifd---qllldr 656
QY 658 A--KGAQASPPPIAPYSPTRKDLLHMOELCEGMKLLASDLDNNRIERLNKVPAPD 715
Db 657 aseqgaevspqmapbhpdpdkdivfmgelcndmkllafldqdnmlrlerlhvpsapd 716
QY 716 V 716
Db 717 V 717

RESULT 10
AAM60724
ID AAM60724 standard; Protein; 729 AA.
XX
AC AAM60724:
XX
DT 02-SEP-1998 (first entry)
XX
DE Human TK2 protein sequence.
XX
KW Human; TK2 protein; TK2-specific activity; phosphorylation; IkappaB;
KW screening; IKB serine 36-specific kinase; TK2-specific binding agent;
KW diagnosis; gene therapy; immunogen.
XX
OS Homo sapiens.
XX
PN US5776717-A.
XX
PD 07-JUL-1998.
XX
PE 17-NOV-1997; 97US-0971937.
XX
PR 07-MAR-1997; 97US-0812533.
XX
PA (TULA-) TULARIK INC.
XX
PI Cao Z;
XX
DR WPI: 1998-398030/34.
XX
DR N-PSDB; AAV36086.
XX
PT New TK2 protein kinase that specifically phosphorylates IkappaB -
PT used to identify modulators of phosphorylation, potentially useful
PT as diagnostic or therapeutic agents
XX
PS Claim 1; Columns 15-18; 12pp: English.
CC The present sequence represents a new human TK2 protein that has
CC TK2-specific activity. The TK2 protein specifically phosphorylates

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CC IkappaB (Ikb), an inhibitor of the NF-kappaB transcription factor,
CC at serine 36. The specification describes a method for screening
CC agents that modulate phosphorylation of Ikb by a kinase (particularly
CC TK) that is specific for Ikb36. The method comprises incubating isolated
CC Ikb serine 36-specific kinase, Ikb serine 36 (substrate) and the test
CC compound, determining the extent of substrate phosphorylation and
CC detecting any alteration of this value by the test compound.
CC The TK2 protein is used to screen for agents that modulate binding of
CC TK2 to its target. TK2-specific binding agents (modulators) are
CC potentially useful for diagnosis (e.g. hybridisation screening for TK2
CC transcripts), in gene therapy to alter TK2 expression, as immunogen, as
CC reagent for isolating other transcription regulators and for screening
CC chemical libraries for candidate drugs.
XX
SQ Sequence 729 AA:

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Query Match 46.8%; Score 1719.5; DB 19; Length 729;
Best Local Similarity 48.3%; Pred. No. 2.5e-136;
Matches 356; Conservative 120; Mismatches 206; Indels 55; Gaps 10;

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QY 1 MOSTAIVYHTDLDLQGAFTASYKARNKSGELVAVKVNTSYLRPREVOREFEYLR 60
Db 1 mgsstshlwlisdllggatanyfrgrhkktdglfakvfnisflrpdvqgmrefevlk 60
QY 61 KLNHONIVKLFAVEETGSGRQKVLVMEVCGSSGLSVLESPPNAGCPDEPLVLRVY 120
Db 61 klnhknivklfaleetctrhkvllmefcpgslvleespanaylpsesellvrlrv 120
QY 121 AGNNHLRENGIVYHRIKPGNINMLVGEESQSYKLTDFGARELDDEKFEVSYTEYTL 180
Db 121 ggmnhlrengivhriidkpgnintmrvgedqsvyktldfgaareldedqfvslygteeyl 180
QY 181 HPDMYERAVLRKPOKAFQVYDLSIGVTLVYHAATGSLPTPEFGSPRRNKEIMRTITE 240
Db 181 hpdmyeravlrkdkqkqyagatvdlwsiyvtfyhaatgsjprfegsprnkemvklitg 240
QY 241 KPAGAJAGQRRNGPLFEMSYTLPTCOLSLGLOSQVPIITANILEVQAOCWGDQFPA 300
Db 241 kpsagalsyqkqenpidsqgmprvscslsrglqvllcpvianlleaadcwgdqfifa 300
QY 301 ETSIDILQRVVHVFSLSQAVLHHIYIHAHNTAIFQEAHVHKTQSVAPRHOEYLFEGHLCV 360
Db 301 etsidilhrvvhvfvslsqavlhhiyihahntaifqeahvhktsvaprhoeylfeghlc 360
QY 361 LEPSVSAOHIAHTTASSPLTLPSTAIPKGLAFRDPALDVPKFPVKYDLADYNTRAKGV 420
Db 361 lepsvsaohiahtasspltlpstaipkglafrdpaladvpkfvpkydoadyntrakgv 420
QY 421 AGYQALRLARALLDQGLMEFGLHWMEVLAQTCRRTL-----EVAFTSL 465
Db 421 wcyacriastlllygelmrkgtlwlleikddynetvhhkktewtlidfcrlmekvk 480
QY 466 LYLSSSLGTERSSVAGTPEIOELKAAAEKLSRLTAEVLSRCSQNTTQESLSINR 525
Db 461 vy-----eklmk--nleaaelgeisdintkrlriss-----sgtlet-slgids 524
QY 526 ELVKS-----RDQVH-EDRSIOOIOCCLDKMFYKQFKSRMRPGLGYNEDQIHK 575
Db 525 rlsppgsjadawahqegthpkrnveklqvllncmteilygfkdkkaerrlayneqihk 584
QY 576 LDKVNFSLAKRLLOVFOECVQKQVQASIVYHGRMRVHETRNHLRLVGCVAACWTEA 635
Db 585 fdkqklythackamchfdcecvkyaefalnseeirkmhrlrlq-----slncgc 637
QY 636 QGVQSSLSKL-----LEELSHQLQDRAKAQASPPPIAPYSPTRKDLLHMOELCEG 689
Db 638 fdleevsvkygeytmelqetlpqkmftassgikhtmpriyp-snatlvemtigmkklkee 696
QY 690 KRLASDLDNNRIER 706
Db 697 mcgvvkeelaemnhlier 713

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XX Claim 1: Fig 8-9, 31pp: English.
 PS The present sequence is human inhibitory kappa B kinase 4 (IKK4).
 CC The IKK4 protein regulates interleukin-8 (IL-8) gene via the
 CC nuclear factor (NF)-kappa B site. The protein is useful for screening
 CC agents with antiinflammatory activity. Modulators of IKK4 is useful for
 CC treatment or prophylaxis of a disorder which is responsive to modulation
 CC of protein activity in a mammal. The IKK4 modulators are particularly
 CC useful for treating diseases involving inflammation and allergies such
 CC as asthma, atopic dermatitis, arthritis, rheumatoid arthritis, systemic
 CC lupus erythematosus, lipopolysaccharide-induced contact dermatitis,
 CC glomerulonephritis and gout. The IKK4 polynucleotide is useful for
 CC preparing probes which are utilized to screen a cDNA or genomic library.
 CC The antibodies against protein are useful for purifying protein or its
 CC portion and to locate the protein in tissue expressing the protein.
 CC Complementary or antisense strands of IKK4 polynucleotide is useful
 CC for gene therapy. The regulatory regions controlling expression of
 CC protein is used in gene therapy to control expression of the therapeutic
 CC construct in cells expressing IKK4 protein.
 CC
 XX Sequence 729 AA;
 SQ
 Query Match 46.8%; Score 1719.5; DB 22; Length 729;
 Best Local Similarity 48.3%; Pred. No. 2.5e-136;
 Matches 356; Conservative 120; Mismatches 206; Indels 55; Gaps 10;
 OY 1 MOSTANVLMHTDDLLGCGTASVYKARKKSGELVAWVFNNTSYLRRENOVREFELR 60
 DB 1 mgsctsnhlwllsdllggatatanvtrgnkkgldfalkvfmisflrvdqmeefevlk 60
 OY 61 KLNHGNIVKLFVAVETGGSRKRVLMVMEYCSSGSLSVLESPENAFGLPEDEFLVLRGV 120
 DB 61 klnhknivklfaieeetttrhkvltmefcpgslytlveepnagylpesellvltv 120
 OY 121 AGMNLRLRENGIVHRDIKGNITRLVGBGQSTYKLTDFGARELDDDEKENVSTGEYL 180
 DB 121 ggmnhlrlrengivhrdtkpnmrvigedqsvyktldfgaareldedegfvslytgeyl 180
 OY 181 HPDMTERAVLRKPOKAGGVVWDLMSIGVTLVHAATGSLPFPEGGPRNKEIWRITTE 240
 DB 181 hpdmteravlrkpoakagvvdwlmstgvtlvhaatgslpfpeggprnkeiwmrkitt 240
 OY 241 KPGAGIAGQRRENGPLEMSYTLPTICOLSLGQSLVPIIANTILEVSCAKMGDFQFPA 300
 DB 241 kpgagisgvgkeengpidsqmpscslsrglyllprvanlleadaekcmwgdqfta 300
 OY 301 ETSDLQRYVNVVVFSLQAVLHHTIAHNTAIFQEVNKHQTSVAPRHQEYLFEGHLCV 360
 DB 301 etsdllhmvvhlvftlqgmthklyihgntatlfheivkyqtkliisngelilygrtlv 360
 OY 361 LEPSVAQHIAHTTASPLTLFSTAIPIKGLAFRDPAIDVPRVVDLZADVNTKKGVLG 420
 DB 361 lepglaqhfkktleemprlfvsvreplntiglyekisipkvpnyddldgdsamakaltg 420
 OY 421 AGYQALRLARALLDGOELMFRLAHMVEVLOATCRRTL-----EVAFTSL 465
 DB 421 vvcyacrilaastllygelmrktgrvltelkodynetvthkkevrltldfcrlmektkv 480
 OY 466 LYLSSLSGTERSSVAGPEIDELAAAEELSRRLTALEVLSRCQNTTEOESLSSNR 525
 DB 466 lylsslsgeressvagrpeidelaalaelksrsltalevlsrscqntteoeslssnr 525
 OY 524 481 vy-----eklmk--lleeaelgeladlnkllrsls-----sgfiet--stqldis 524
 DB 524 481 vy-----eklmk--lleeaelgeladlnkllrsls-----sgfiet--stqldis 524
 OY 526 ELVKS-----RDQVH-EDRSIOIOCCLDKMNFIYKOPKSRMRPGGLGYNEQIHK 575
 DB 526 rlspggsiadavahqegchpkdrnveklqvlncmteilyqfkkaerrlayneeqlnk 584
 OY 576 LDKVNFSLAKRLQVFOECVQYQASLVTHGRMRVHETRNMLRVGGSVAACNTEA 635
 DB 576 ldkvnfslakrlqvfocvqyqaslvthgrmrvhetrnmlrvvggsvaacntea 635
 OY 635 585 fdkglylthakamchfdcevkkyeaflnkseewlrkmlhrlkql-----istnqc 637
 DB 635 585 fdkglylthakamchfdcevkkyeaflnkseewlrkmlhrlkql-----istnqc 637
 OY 689 636 QGVQESLSKL-----LEELSHQLQDRAKGAQASPPRIAPPPSTRKDLIMQELCEG 689

DB 638 fdieevskkygeynelqetlpgkfmfssgikhtmtlpy-psntlvmwlmgmkkikee 696
 OY 690 MKLLASDLDDNNRIER 706
 DB 697 megvkvlaennhllr 713
 RESULT 14
 AAB65601
 ID AAB65601 standard; Protein: 729 AA.
 AC AAB65601;
 XX 27-MAR-2001 (first entry)
 DE Novel protein kinase, SEQ ID NO: 126.
 XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiaslomatic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
 OS Homo sapiens.
 XX WO200073469-A2.
 PN 07-DEC-2000.
 PD 26-MAY-2000; 2000WO-US14842.
 PF 28-MAY-1999; 99US-0136503.
 PR (SUGEN-) SUGEN INC.
 PA Plowman GD, Martinez R, Whyte D, Sudarsanam S;
 PI WPI: 2001-032161/04.
 DR N-PSDB: AAF44626.
 XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers -
 PS Claim 10; Fig 1; 31pp: English.
 PS The present sequence is a novel protein kinase. The novel protein kinases
 CC and the nucleic acids that encode them may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiovascular diseases, strokes, renal failure,
 CC oxidative-stress related disorders, chronic inflammatory bowel disease,
 CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
 CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
 CC reproductive disorders.
 XX Sequence 729 AA;
 SQ
 Query Match 46.8%; Score 1719.5; DB 22; Length 729;
 Best Local Similarity 48.3%; Pred. No. 2.5e-136;
 Matches 356; Conservative 120; Mismatches 206; Indels 55; Gaps 10;

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QY 1 MOSTANTLMTDLDLGGATASVYKARKKSGELVAVKVNTSTYLRPREVOVREFEVL 60
DB 1 mgsstnhlwl1sdlllgqatanvfrgrhkktdglfaikvfnnisflrpdvqmfefevlk 60
QY 61 KLNHONIVKLFVAVETGGSRKVLVMEYCGSSGLSLVLESPENAFGLPEDEFLVLRGV 120
DB 61 klnhknivklfaieettrkhvllmeifcpgslylvleesnaaylpeeseflilvdrvv 120
QY 121 AGMNLRENGIVHRDIPKGNIMRLVGEOSIYKLTDFGAARELDDDEKVFVSYTEEYL 180
DB 121 gsmnhlrengivhrdipkgnimrvlgedgsyvkltfdgaarelededqfvslygteeyl 180
QY 181 HPDMYERAVLRKPOQKAFGVTVDLMSIGVTLVHAATGSLPIRPFEGPRRKEIMYRTTE 240
DB 181 hpdmyeravlrkdhqkkygatvdlwsgvltfhaatgsldpfrfegprnrkewmykiltg 240
QY 241 KPAGIAGAOBRENGPLEWSTYLPITQOLSLGLOSOLVPLANTLILVEQAOKMGFOFEFA 300
DB 241 kpgaisgvgkaengpldwsgdmpscslsrglqvlllpvianlleadqekcwqldqfifa 300
QY 301 ETSDLQRVVAVHVESLSQAVLHHIYIHAHNTAIFOEAVHKOTSVAARHOEYLFEGHLCV 360
DB 301 etsdlhmvavhveslsgmtahkiyhsyntatfihelykqtklissngelilyegrrlv 360
QY 361 LEPVSQAQIHATHTASSPDLTFFSTAIKGLAFRDPALDVPKVPKVDLQADYNTAKGVLG 420
DB 361 lepgrlaqhpktteempifvrsreplntlylgyekislkvhpryldgdasmakaitg 420
QY 421 AGYQALRARALRDLGOELMFRGLHVMVEVLOATNCRTL-----EVATSL 465
DB 421 vgcactiaastlilygelmrkgrlwllellkddynevhvkktevalldfcitnlektvk 480
QY 466 LYLSSSLGTERFSSVAGTPLEIOELKAAELRSRLTAELVLSRCSQNTITEOSTSLSLNR 525
DB 461 yy-----eklmki--nleaeelgeislhtklrliss-----sgqtlet--slqids 524
QY 526 ELVYS-----RDQVH--EDRSIQIOICCLDMANTYIOFKFSRRRPGGLGNEEOIHK 575
DB 525 rlspsgsldawahqegthpdriveklqylhncmteilygyfkkdkaeerllyneegqihk 584
QY 576 LDKVNFSLHAKRLIQVFOEBCVOKYQASIVYHGRMRVHETRNHLVLCGSAACNTFA 635
DB 585 fdckklyllyhatkamhtidcevkvkyaeflnkseeirkmhlhtkql-----lslngc 637
QY 636 QGVQESLSKL-----LEELSHQLLDQRAGQAQASPPPIAPYPSPTRKDLILHMOELCEG 689
DB 638 fdteeevskygeytnelgetlpqkmftassgikhtmprip-ssntivemtlgmakklkee 696
QY 690 MKLASLDLNNRIIER 706
DB 697 megyvkeelaennhiller 713

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RESULT 15

AAV80280
ID AAV80280 standard; Protein; 729 AA.

AAV80280;

26-MAY-2000 (first entry)

Murine I kappa B kinase-related kinase 2 SEQ ID NO:4.

Mouse; murine; I kappa B kinase-related kinase; IKR-1; IKR-2;

protein kinase; immunomodulatory; antiinflammatory; antimicrobial;

cytostatic; autoimmune; inflammatory; infection; neoplastic disease.

Mus sp.

WO200008179-A1.

17-FEB-2000.

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PF 04-AUG-1999; 99WO-US17578.
XX 04-AUG-1998; 98US-0095269.
PR 11-SEP-1998; 98US-0099973.
PR 05-FEB-1999; 99US-0118783.
XX (IMMUNEX CORP.
XX
XX Bird TA, Virca GD;
XX WPI, 2000-195583/17.
DR N-PSDB; AA295276.
XX
XX Novel kappa B-kinase related kinases IKR-1 and IKR-2 used as molecular
XX weight markers and in peptide fragmentation studies
XX
XX Claim 13; Fig 4; 85pp; English.

```

The present sequence represents murine I kappa B-kinase related kinase 2 (IKR-2). IKR proteins have immunomodulatory, antiinflammatory, antimicrobial and cytostatic activities. IKR polynucleotides can be used to express the proteins, and as probes to identify nucleic acids encoding proteins having kinase activity. IKR-1 and IKR-2 proteins and fragmented polypeptides are used for purifying proteins, e.g. to purify binding partner proteins; to measure protein activity, e.g. as quality assurance agents to monitor shelf life and stability of binding partner proteins. They may also be used as research agents, e.g. in assays to determine protein kinase activity, to identify novel molecules involved in signal transduction pathways, and to identify therapeutic compounds, to identify substances which interfere with the rate of substrate phosphorylation (such compounds would be useful for the treatment of autoimmune, inflammatory, infectious or neoplastic diseases), as molecular weight and isoelectric focusing markers, as controls for peptide fragmentation, identification of unknown proteins, e.g. by comparison with proteins in databases and for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunoprecipitation chromatography. The antibodies can also be used to block binding of the IKR polypeptides to their binding partners.

Sequence 729 AA:

Query Match 46.6%; Score 1710.5; DB 21; Length 729;
Best Local Similarity 48.6%; Pred. No.1.5e-135;
Matches 352; Conservative 119; Mismatches 224; Indels 29; Gaps 7;

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QY 1 MOSTANTLMTDLDLGGATASVYKARKKSGELVAVKVNTSTYLRPREVOVREFEVL 60
DB 1 mgsstnhlwl1sdlllgqatanvfrgrhkktdglfaikvfnnisflrpdvqmfefevlk 60
QY 61 KLNHONIVKLFVAVETGGSRKVLVMEYCGSSGLSLVLESPENAFGLPEDEFLVLRGV 120
DB 61 klnhknivklfaieettrkhvllmeifcpgslylvleesnaaylpeeseflilvdrvv 120
QY 121 AGMNLRENGIVHRDIPKGNIMRLVGEOSIYKLTDFGAARELDDDEKVFVSYTEEYL 180
DB 121 gsmnhlrengivhrdipkgnimrvlgedgsyvkltfdgaarelededqfvslygteeyl 180
QY 181 HPDMYERAVLRKPOQKAFGVTVDLMSIGVTLVHAATGSLPIRPFEGPRRKEIMYRTTE 240
DB 181 hpdmyeravlrkdhqkkygatvdlwsgvltfhaatgsldpfrfegprnrkewmykiltg 240
QY 241 KPAGIAGAOBRENGPLEWSTYLPITQOLSLGLOSOLVPLANTLILVEQAOKMGFOFEFA 300
DB 241 kpgaisgvgkaengpldwsgdmpscslsrglqvlllpvianlleadqekcwqldqfifa 300
QY 301 ETSDLQRVVAVHVESLSQAVLHHIYIHAHNTAIFOEAVHKOTSVAARHOEYLFEGHLCV 360
DB 301 etsdlhmvavhveslsgmtahkiyhsyntatfihelykqtklissngelilyegrrlv 360
QY 361 LEPVSQAQIHATHTASSPDLTFFSTAIKGLAFRDPALDVPKVPKVDLQADYNTAKGVLG 420
DB 361 lepgrlaqhpktteempifvrsreplntlylgyekislkvhpryldgdasmakaitg 420

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 14, 2002, 17:33:33 ; Search time 67.53 Seconds
(without alignments)
256.977 Million cell updates/sec

Title: US-09-582-397A-2

Perfect score: 3674
Sequence: 1 MOSTANVLMHTDLDLGGAGAT.....LLDNNRIETRLNRPAPPDV 716

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Dackfil1est1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1719.5	46.8	729	1	US-08-971-937-2
2	1719.5	46.8	729	2	US-08-812-533-2
3	424	11.5	756	2	US-08-887-518-4
4	424	11.5	756	2	US-09-023-321-4
5	424	11.5	756	2	US-08-890-853-2
6	424	11.5	756	2	US-09-032-475-4
7	424	11.5	756	2	US-09-099-1254-2
8	424	11.5	756	2	US-09-099-1254-2
9	424	11.5	756	4	US-09-032-476-2
10	424	11.5	756	4	US-08-890-854-2
11	424	11.5	756	4	US-09-023-324-2
12	424	11.5	756	4	US-09-168-629-15
13	424	11.5	756	4	US-08-910-820-9
14	394	10.7	745	2	US-08-887-518-3
15	394	10.7	745	2	US-09-023-321-3
16	394	10.7	745	2	US-09-032-475-3
17	394	10.7	745	4	US-09-168-629-2
18	394	10.7	745	4	US-08-910-820-10
19	394	10.7	745	4	US-08-810-131A-2
20	391	10.6	745	2	US-08-890-853-4
21	391	10.6	745	2	US-09-099-1254-4
22	391	10.6	745	2	US-09-099-1254-4
23	391	10.6	745	4	US-09-032-476-4
24	391	10.6	745	4	US-08-890-854-4
25	391	10.6	745	4	US-09-023-324-4
26	379	10.3	584	3	US-09-160-483-1
27	305.5	8.3	582	4	US-09-428-711A-2

28	305.5	8.3	1051	4	US-09-428-711A-14	Sequence 14, Appl
29	303.5	8.3	1050	4	US-09-428-711A-16	Sequence 16, Appl
30	303	8.2	1037	4	US-09-428-711A-21	Sequence 21, Appl
31	296	8.1	647	3	US-09-031-563-7	Sequence 7, Appl
32	296	8.1	1315	3	US-09-031-563-2	Sequence 2, Appl
33	296	8.1	1315	4	US-09-293-505-10	Sequence 10, Appl
34	294	8.0	454	2	US-09-159-385-1	Sequence 1, Appl
35	294	8.0	454	4	US-09-186-277-1	Sequence 1, Appl
36	294	8.0	1315	3	US-09-031-563-25	Sequence 25, Appl
37	292	7.9	648	3	US-08-677-298-2	Sequence 5, Appl
38	290.5	7.9	729	2	US-08-677-298-2	Sequence 2, Appl
39	282	7.7	260	3	US-09-031-563-24	Sequence 24, Appl
40	276	7.5	776	1	US-08-198-446B-17	Sequence 17, Appl
41	276	7.5	776	2	US-08-870-693-17	Sequence 17, Appl
42	276	7.5	821	1	US-08-198-446B-6	Sequence 6, Appl
43	276	7.5	821	2	US-08-870-693-6	Sequence 6, Appl
44	274	7.5	201	3	US-09-124-476-2	Sequence 2, Appl
45	274	7.5	201	4	US-09-577-796A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-971-937-2
Sequence 2, Application US/08971937
Patent No. 5776717
GENERAL INFORMATION:
APPLICANT: Cao, Zhaoan
TITLE OF INVENTION: TRAF2-Associated Kinase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,937
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/812,533
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-971-937-2

Query Match 46.8%; Score 1719.5; DB 1; Length 729;
Best Local Similarity 48.3%; Pred. No. 6.9e-146;
Matches 356; Conservative 120; Mismatches 206; Indels 55; Gaps 10;
QY 1 MOSTANVLMHTDLDLGGAGATASYKARNKSGELVAVKVFNTTSYLRRPREVQREFEVLK 60
DB 1 MOSTSNHMLSDILGGAGATANYFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREREVLK 60

[illegible]

RESULT 3
US-08-887-518-4
Sequence 4, Application US/08887518
Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-4

Query Match 11.5%; Score 424; DB 2; Length 756;
Best Local Similarity 23.2%; Pred. No. 2e-29;
Matches 181; Conservative 123; Mismatches 325; Indels 150; Gaps 25;
QY 9 WHTDLLGQATSVYARAKKSGELVAVKVFNTTSLRPREVQVREVEVLKRNHONY 68
DB 15 WEMKERLGTGGFGVNVIRHNDTEBOIAIKOCROELSPRNERWCLEIOMIRLTHPNV 74
QY 69 KLFVVEE---TGGSRQKLVNVEYCSSGLSLVLESPENAFGLPEDEFLVLRGVVAGMN 124
DB 75 AARVPPEGMOLAPNDLPFLAMEYCGGDLRKYLNOFENCCGLAREGALITLISDIASLR 134
QY 125 HARENGIVHRDIKPGNIMRLVLEGQSIYKLTDFGARELDDDEKFNVSVGTETEEYLPDM 184
DB 135 YLHENRITHRDLKRENVILOQGEQ-RLTHKRIIDLYAKELDQGSLSFVGTQLYAPEL 193
QY 185 YERAVLRKPOKAGVYVDLMSIGVTLNATGSLPFPFGP-----RRNEIMWRI 237
DB 194 LE-----OQYTVVDWVSFGTLAECLTGERPFLPNNOPOVMKSVKQKSEVDIV 245
QY 238 TTERFAGAIAGQRENGPLMESYTLPTICQLSLGSLQSLVPIIANILEVEQAK-----C 292
DB 246 SEDL-----NCTVAFSSSLYPVNNLSVLARLEKMIQLMLMWHPRQGTDP 293
QY 293 WGFDOFPAETSDIOLRVVYVPSQAVLHNIYHAHTIAIFQPAVYKQSVAPRHEV 352
DB 294 YGPNCGCFRALDDIILNKLVLHLMVGTGTHYPTVEDSLQSLKRIQDDTGIPREDEL 353
QY 353 LFEGLVLEPVSVAOHIA-----HTTASGPLTLFSTA-----IPKGLA-- 391

DB 354 IQEAGLALIPDKPATQCSIDCKLNEGHTLDMDLVFLFONSKITYETQISPRPPQESVSCI 413
QY 392 FDDPALDVPKE-VPKV-----DLQADYNTAKGVLAGAGQALRLARALLDQOELMR 441
DB 414 LOEPRNLAFQLRKVMQVWHSIOTLKEDCNRLQ-----QGRRAAMMLLRNNSCLS 466
QY 442 GLHWMEVLQATCRRTLEAVARTSLYSSISCTERFS-----SVAGTPEI--OELKAA 493
DB 467 KKNMSASKSOOLKAKLDEFKSTI-----QIDLEKYSQTERGISDQLLAWREMEQAV 521
QY 494 ELRSR--LRTLAEVLSRCSQITETQES-----LSSNRELV-----KSDQ 533
DB 522 ELGRENEMKLLVERMMALQTDIVLOSPPMKRGKGTLDLEQARELYRLAREKPRDQ 581
QY 534 VHEDS-----IQIOCCLDKMFITYKQFKSHMRPGLGYNEQIHKLDKVNFSHLAK 586
DB 582 RTEGDSQEWKRLLOLQISFEKKVITYQLSKT-----VCKQKALELPV----- 629
QY 587 RLQVFOEBCVOKYQASLVYTHGRMRKRVHETRNHLVGCVAACNT---EAQVOESLS 643
DB 630 -----EVV-----SLNNEDEKTVRLQEKROKELMNLKIASKVGVPVSGSPDSMN 677
QY 644 KLEEISHLQDRKAGAAQAPPPPIAPYSPTRKDLLHMOELCEGMKLLASDLLDNNR 702
DB 678 ASRLSQPGQIMSQPSTASNS-----LPEPAKSEELVABAHNLC--TLLENALQDPYR 728

RESULT 4
US-09-023-321-4
Sequence 4, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Roche, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-023-321-4
Query Match 11.5%; Score 424; DB 2; Length 756;

RESULT 5
 US-08-890-853-2
 : Sequence 2, Application US/08890853
 : Patent No. 5851812
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Goeddel, David V.
 : APPLICANT: Woronicz, John
 : TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 : NUMBER OF SEQUENCES: 4
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 : STREET: 268 BUSH STREET, SUITE 3200
 : CITY: SAN FRANCISCO
 : STATE: CALIFORNIA
 : COUNTRY: USA
 : ZIP: 94104
 :
 : COMPUTER READABLE FORM:

Query Match	11.5%	Score 424;	DB 2;	Length 756;
Best Local Similarity	23.2%	Pred. No. 2e-29;		
Matches 181;	Conservative 123;	Mismatches 325;	Indels 150;	Gaps 25

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0Y 9 WHPDDLLGGGAATASYKANKKSSGELVAVKYNNTTSYLRPREVOYREFEVLKLNHONIV 68
Db 15 WEKKEKLTGGGEGNATLRMHNQETGQIAKOCROELSPNNRRMCELOIOMRLTHHPVV 74
0Y 69 KLEFAYEE----TGSSROKLVMEGSSGSLSVLESPENAFGLPEDEFLVYRCVVAGMN 12
Db 75 AARDVEGQONLAPNDLPLLAMEYOGGDLKRYLQNFENCCGLRGAGLITLSDIASLR 13
0Y 125 HLRENGIYHRDIPKGNIMLVGEEQOSIYKLTDFGARELDDDEKFSVYSTEELYHPDM 18
Db 135 YLHENTLIHRDLKPEVITYAQOEO--RLHKIIDLYAKELDQSGISCTSPVGTLYQVAPEL 19
0Y 185 YERAVLRKPOQKAFQYVDLMSIGTLYHAAAGSLPFIPIPGP-----RRNKEIMRI 23
Db 194 LE-----QQKYVYVDYMSFGFLAEECTIGFERPELRNMQPOVMSKVAOKSEVDIV 24
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Db 246 SBDL-----NCTVWSSSLPYPRNNLSVLARELKEWLOLMLMNHPRQGRDPT 29
0Y 293 WQFDQFPAFTSDILQVYVAVHFSLSQAVLHHIYIHAHNTIYLPOEAVYHKQTSVAPRQEV 35
Db 294 YQPNCCFRAKLDILMLKVLHIMVTGITHIYRYVEDESLOSILARIQDGTGIEEDQEL 35
0Y 353 LEFGHLVLEPSVSAQHTA-----HTTASSPLTLESTA-----IPKGLA-- 39
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0Y 392 FRDPLADVPKF--VYPV-----DLQADNYTKVGLGAGYQALRLARALLDQELMFR 44
Db 414 LOEPKRNIAFOLKRWKVCQVHNSIOTLKECDNRQO-----QOORAMNNLLRNNSCLS 46
0Y 442 GLHWMEVYLQATCRRTLEVARTSLIYVSSLSIGTERFS-----SVAQPEI--OELKAA 49
Db 467 KKNKSMASMSQOLKAKIDFEFTSI-----QIDLEKYSQTEFEGTTSKLLANREMQAV 52
0Y 494 ELRSR--LRLLAEYLSKCSQNTTETORS-----LSLSNRELY-----KSRQ 53
Db 522 ELCCGENEVKLLVERMALQTDIYDLORSPIGRKQCGSTLDDLEBOARELYRLREKPRQ 58
0Y 534 VHEDESS-----LOOIOCCLDKNMFIYKQFKFSRMRPGLGUYNEQJHKLDKYVNSHLAK 56
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OY 587 RLLOFQECVQKYOASLVTHGKRMRYVHETRNHLRLVGSVAACNT---EAQGVQESLS 643
DB 630 -----EEVY-----SLMNEDEKTVRLQEKROKELMNLKICSVYRGVSGSPDSMN 677
OY 644 KLEELSHOLLQDRAKGAQSPPIAPYPSPTRKDLLHMOELCEGKMLASDLLDNRR 702
DB 678 ASRLSOPQOLMSOPSTASNS-----LPEPAKSEELVAEAHNLIC---TLENAIOTDVR 728

RESULT 6

US-09-032-475-4
Sequence 4, Application US/09032475
Patent No. 5854003
GENERAL INFORMATION:
APPLICANT: Rothe, Mike
APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032.475
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-032-475-4

Query Match 11.58; Score 424; DB 2; Length 756;
Best Local Similarity 23.2%; Pred. No. 2e-29;
Matches 181; Conservative 123; Mismatches 325; Indels 150; Gaps 25;

OY 9 WHTDLLQSGATASYKARKNKSGELVAVKFNNTSYLRPREVQVREVEYRKLNHONIV 68
DB 15 WEMKRRLTGCGNVIYRHNHNOETGQOIAIKQCRQRLSPRRNRKWLCTQIMRKLTHPVV 74
OY 69 KLFAYEE---TGSRQKVLVMEYSSGSLSVLESPENAFGLPDEFLVYLRCVAGMN 124
DB 75 AARDVEGQMONLAPNDLPLAMEYCGGDLRKYLNOFENCGSLREGAILTLISDIASALR 134
OY 125 HIRENGIYHRDLPKGNIMRLVGEBOGSIYKLTDFCAARELDDEKFEVYVYGEELHADM 184
DB 135 YLHERRIIRHDLKPNIVYLOQEO-RLIHKIIDLGVAKELDQGLCTSEFVGLIYLAEL 193
OY 185 YRAVLRRPQKAFGVYDLMISIGVLYHAATGSLFIFPGP-----RNRKIMYRI 237
DB 194 LE-----QOKYIVYDYMSFGTLAEFCITGFRPFLPNMOPVOMHAKVOKSEVDIV 245

OY 238 TTEKPAIAGAOBRNGPLEMSTYLRITCOLSLGLOSQVLPILANILEYQAK-----C 292
DB 246 SEDL-----NGYKFESSLIPYRNINLSVLAERLEKQLQMLMHNRRQSTDP 293
OY 293 WGDQFEAETSDILQRYVNVFSLQAVLNHYIHAHNTAITPOEAVNHKOTVAPRHOEX 352
DB 294 YGPGCEKALDILNLEKTLILNVTGTIHTYPTVEDESISIKARIQOTGTIPREDEQL 353
OY 353 LFECHLCVLEPVSQAQIIA-----HTTASSPLLEFSTA-----IPKGLA-- 391
DB 354 LQEGALALIPDKPATOCISDGKLNKGHTLDMDLVFLFDNSKITVEQISRPQPEVSCI 413
OY 392 FRPDALVPRF-VPKV-----DLQADYNTAKGVLAGYQALRLARLALGOELMFR 441
DB 414 LQPKRLAFAFQKRWGQVWHISQTLKECQNLQ-----OGQRAAMNLRNNSCLS 466
OY 442 GLHWMEVLOATCRRLTLEVARTSLLYSSSLGTERES---SVAGTPEI---QELKAA 493
DB 467 MKKSMASMSQOLKAKIDPFKTSI-----QIDLEKYSQTEFGITSDKLLAWREMOAV 521
OY 494 ELKSR---LRTLAEVLSCQNTITEOS-----LSLNRELY-----KSROQ 533
DB 522 ELGRENEMKILVERMMAIOTDVLQRSMPGRKQGGTLDLEQARELYRLRREKPRD 561
OY 534 VHEDRS-----IQOIOCLDKMNFYKOPKSRMRPGLYNEEOIHKDKYFESHAK 586
DB 582 RTEGDSQEMVRLLOAQSEKVKRYIYIOLSKT-----VYCKQKALELPKV----- 629
OY 587 RLLOFQECVQKYOASLVTHGKRMRYVHETRNHLRLVGSVAACNT---EAQGVQESLS 643
DB 630 -----EEVY-----SLMNEDEKTVRLQEKROKELMNLKICSVYRGVSGSPDSMN 677
OY 644 KLEELSHOLLQDRAKGAQSPPIAPYPSPTRKDLLHMOELCEGKMLASDLLDNRR 702
DB 678 ASRLSOPQOLMSOPSTASNS-----LPEPAKSEELVAEAHNLIC---TLENAIOTDVR 728

RESULT 7

US-09-099-125A-2
Sequence 2, Application US/09099125A
Patent No. 5916760
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099.125A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/890,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342

; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 756 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-099-125A-2

Query Match 11.5%; Score 424; DB 2; Length 756;
 Best local similarity 23.2%; Pred. No. 2e-29;
 Matches 181; Conservative 123; Mismatches 325; Indels 150; Gaps 25;

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OY 9 WHTDLLGOGATASYKARKKSGELVAVKVFNTSYLRPREVOYREFEVLRLKLNHONY 68
DB 15 WEKRLGTGGFGVNIIRHNGETGEQIAIKQCRQELSPRNERMCKLEIQIMRLHNPV 74
OY 69 KLFAYE-----TGGSKQVLYMEYCSGSLSVLESPENAFGLPDEFLVLRVYAGM 124
DB 75 AARDVEGMQNLAPNDLPFLAMEYCOGDLRKYLNOFENCCLRGAILTLSDIASALR 134
OY 125 HLRENGIYHRDIKPGNIMRLVGEESGIYKLDFGAARELDDEKRVSYGTEEYLHPDM 184
DB 135 YLHNRITIRDLKRPENIVLQGEQ-RLHKITIDIGYAKELDQSLCTSEVGTQYLAPEL 193
OY 185 YERAVLRKQOKAFGVTVDLMSIGVTLVHAATGSLPTFPFGP-----RRNKEIMYRI 237
DB 194 LE-----QOKYTVTVDMYSFGTLAFECITGFRPFLPNMQPVGMHKSVMKSEVDIV 245
OY 238 TTEKPAIALAGAKORRENGLEMSYTLPTQCLSLGLOSQVLPITANILEVQAK-----C 292
DB 246 SEDL-----NGTVFSSSLPPNNLNSVLAERLEKWLQMLMHPROGTDPT 293
OY 293 WGFDOFFAETSDILORVVHVFSLOAVLHNTIYIAHNTIAIFQEAHVHKTQSVAPRHOEX 352
DB 294 YGPGCGFKALDDLNLKLVHLNMVGTGITHRYPTEDESLQSLKARIQODTGIPEDDEL 353
OY 353 LFEGLCVLEPSVSAOHIA-----HTTASSPLTLFSTA-----IPKGLA-- 391
DB 354 LOEAGLALIPDKPATOCISDGKLNKGHTLMDLVLFNDSKITVEYEQISPPROPESVSCI 413
OY 392 FRDALDVPKF--VPRV-----DLQADYNTAKGVLAGYQALRLARALLDGOELMFR 441
DB 414 LOEKRNIAFQILKRWGQVHNSIQTLKEPCNRLQ-----QGRAMMNLNNSCLS 466
OY 442 GLHVMVLAQTCRRITLEVARTSLYLSSLSGTERFS-----SVAGTPEI--OELKAA 493
DB 467 KMKNSMASMSQOLKAKIDFEKTSI-----QIDLEKYSQGEFEGITSDKLLAMHEMQAV 521
OY 494 ELRER-----LRTIAVLSRCSNITEPDS-----LSSLNRELY-----KSRDQ 533
DB 522 ELGRENVEVKKLVERMALQTDIVDILQSRPMGRKGGTLDLDEQARELYRLREKPRDQ 581
OY 534 VHEDRS-----TQIOTCCLDKNFTYKOPKSRMRPGLGVNEOIHKIDKNFSLAK 586
DB 582 RTEBDSQEMRLLQALQSEKKRVITYQLSKT-----VYCKQKALELPKY----- 639
OY 587 RLQVQEECVQKYQASLVTHGKRMRYVHETRNHLRLVGSVAACT--EAQVQESIS 643
DB 630 -----EEVY-----SLMNEDEKTVRLQEKROKELMNLKTIACSVRPGVSGPSDM 677
OY 644 KLEELSHOLLQDRAKQASPPRIAPSPTRKDLLHMQELCEGKLLASDLLDNRR 702
DB 678 ASRLSQGLMSOPSTASNS-----LPEPAKSEELVAEAHNLC-----TLENAIODTVR 728
  
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RESULT 8
 ; US-09-099-124A-2
 ; Sequence 2, Application US/09099124A
 ; Patent No. 5939302
 ; GENERAL INFORMATION:
 ; APPLICANT: Goeddel, David V.

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; APPLICANT: Moronicz, John
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,124A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-099-124A-2
  
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Query Match 11.5%; Score 424; DB 2; Length 756;
 Best local similarity 23.2%; Pred. No. 2e-29;
 Matches 181; Conservative 123; Mismatches 325; Indels 150; Gaps 25;

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OY 9 WHTDLLGOGATASYKARKKSGELVAVKVFNTSYLRPREVOYREFEVLRLKLNHONY 68
DB 15 WEKRLGTGGFGVNIIRHNGETGEQIAIKQCRQELSPRNERMCKLEIQIMRLHNPV 74
OY 69 KLFAYE-----TGGSKQVLYMEYCSGSLSVLESPENAFGLPDEFLVLRVYAGM 124
DB 75 AARDVEGMQNLAPNDLPFLAMEYCOGDLRKYLNOFENCCLRGAILTLSDIASALR 134
OY 125 HLRENGIYHRDIKPGNIMRLVGEESGIYKLDFGAARELDDEKRVSYGTEEYLHPDM 184
DB 135 YLHNRITIRDLKRPENIVLQGEQ-RLHKITIDIGYAKELDQSLCTSEVGTQYLAPEL 193
OY 185 YERAVLRKQOKAFGVTVDLMSIGVTLVHAATGSLPTFPFGP-----RRNKEIMYRI 237
DB 194 LE-----QOKYTVTVDMYSFGTLAFECITGFRPFLPNMQPVGMHKSVMKSEVDIV 245
OY 238 TTEKPAIALAGAKORRENGLEMSYTLPTQCLSLGLOSQVLPITANILEVQAK-----C 292
DB 246 SEDL-----NGTVFSSSLPPNNLNSVLAERLEKWLQMLMHPROGTDPT 293
OY 293 WGFDOFFAETSDILORVVHVFSLOAVLHNTIYIAHNTIAIFQEAHVHKTQSVAPRHOEX 352
DB 294 YGPGCGFKALDDLNLKLVHLNMVGTGITHRYPTEDESLQSLKARIQODTGIPEDDEL 353
OY 353 LFEGLCVLEPSVSAOHIA-----HTTASSPLTLFSTA-----IPKGLA-- 391
DB 354 LOEAGLALIPDKPATOCISDGKLNKGHTLMDLVLFNDSKITVEYEQISPPROPESVSCI 413
OY 392 FRDALDVPKF--VPRV-----DLQADYNTAKGVLAGYQALRLARALLDGOELMFR 441
  
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DB 414 LQPKRNLAFFQRLKRWGVWHSIOTLKEDCNRLQ-----QGQRAAMNLLRNNSCLS 466
 QY 442 GLHVMVEVLQATCRRLTEVARTSLYLSSLSGTERPS-----SVAGTPEI---QELKAA 493
 DB 467 KMKNSMASHQOLKAKLDFPKTSI-----QIDLEKXSEOTEGTISDKLLAMREMOAV 521
 QY 494 ELRSR---LRTLAELVSRCSQNTTEQES-----LSSLRRELV-----KSRQO 533
 DB 522 ELGGRNEVKLLVERMALQTDIVDLQSRSPGKRGOGTLDLDEQARELYRLRREKPRQO 581
 QY 534 VHEDRS-----LQOIOCCLDKMFYKQFKSRMRPGIAGVNEBOIHKLDKVNFSHLAK 586
 DB 582 RTEGDSQEMVRLLOAIQSEFEKVRVITYQLSKT-----VVCOKALELPIV----- 629
 QY 587 RLQVFOEBCVQKQASLVTHGKRMVYHETRNHLRVGCSVAACNT---EAGQVQESLS 643
 DB 630 -----EEVY-----SLNMEDEKTVVRLQEKROKELMNLKJACSKVRGPGVSGSPDSMN 677
 QY 644 KLEELSHOLLQDRAKGAQASPPPIAPYPSPTRRDLLHMQELCEGMKLLASDLDDNNR 702
 DB 678 ASRLSOPGQLMSOPSTASNS-----LPEPAKSEELVAEAAHNLIC---TLEENAIQDTYR 728

RESULT 9

US-09-032-476-2
 ; Sequence 2, Application US/09032476

Patent No. 6235492

GENERAL INFORMATION:

APPLICANT: Roche, Mike

APPLICANT: Cao, Zhaodan

TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/032.476

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/890,854

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 797-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 756 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-032-476-2

Query Match 11.5%; Score 424; DB 4; Length 756;
 Best Local Similarity 23.2%; Pred. No. 2e-29;
 Matches 181; Conservative 123; Mismatches 325; Indels 150; Gaps 25;

QY 9 WHTDLDLGATASYKARKNKSGELVAVKVNTTSYLRPREVQREPEVLKLNHONIV 68
 DB 15 WEMKERLGTGCGVNTIRHMQETGEQIAIKOCROELSPRNRRMCLQIOMRLTHPVV 74
 QY 69 KLPAAVE-----TGSRQKVLVMEYCCSSLSLVLESPENARGLPDEFLVYLRCVVAAMN 124
 DB 75 AARDPEGMQNLAPDLPLAMEYCOGGBLRRKYLQFENCCGLRGAILTLLSDIASLR 134
 QY 125 HLRNGIVHROIKPGNIMLVGEEGOSYKLPDFGARELDDEKFEVSYGTEEYLPDM 184
 DB 135 YLHFNRIHRLDKPENITVLOQGEQ-RLHKITIDLGAKRLDQSGICTSVGTLQYLABEL 193
 QY 185 YERAVLRKPOKAFVTVYDLSIGVLYHAATGSLPIFEGP-----RKNKEIMTRI 237
 DB 194 LE-----QOKYTVTVYMSFGTLAFECITGFEPFLPMQPVOMHNSKVRQSEVDIV 245
 QY 238 TTEKPGALAGADRRNGLEWSTYLPICQSLGLOSLQVLPILANILEVQAK-----C 292
 DB 246 SEDL-----NGTVKFSSSLPPNNLNSVLAERLEKWLQMLMWHNRQGTDP 293
 QY 293 WGFDFEAFETSDILQHVHVVSLSQAVLHNYIYHAHTIATFOEAVHKOTSVAAPHQY 352
 DB 294 YCPNGCFKALDILNLKVLHLMVGTIHTYVTEDESISQIKARIQODTGIPEDQL 353
 QY 353 LPEGHLCVLEPVSVAQHIA-----HTTASSPLTLESTA-----IPKGLA-- 391
 DB 354 LQEAGLALIPDKPATQICISDKLNEGHTLDMDLVFLPDKSKITVETQISPRQPEVSQ 413
 QY 392 FRDPALDVPKF-VPKV-----DLQADYNTAKGVLAGYQALRLARALDGOELMR 441
 DB 414 LQPKRNLAFFQRLKRWGVWHSIOTLKEDCNRLQ-----QGQRAAMNLLRNNSCLS 466
 QY 442 GLHVMVEVLQATCRRLTEVARTSLYLSSLSGTERPS-----SVAGTPEI---QELKAA 493
 DB 467 KMKNSMASHQOLKAKLDFPKTSI-----QIDLEKXSEOTEGTISDKLLAMREMOAV 521
 QY 494 ELRSR---LRTLAELVSRCSQNTTEQES-----LSSLRRELV-----KSRQO 533
 DB 522 ELGGRNEVKLLVERMALQTDIVDLQSRSPGKRGOGTLDLDEQARELYRLRREKPRQO 581
 QY 534 VHEDRS-----LQOIOCCLDKMFYKQFKSRMRPGIAGVNEBOIHKLDKVNFSHLAK 586
 DB 582 RTEGDSQEMVRLLOAIQSEFEKVRVITYQLSKT-----VVCOKALELPIV----- 629
 QY 587 RLQVFOEBCVQKQASLVTHGKRMVYHETRNHLRVGCSVAACNT---EAGQVQESLS 643
 DB 630 -----EEVY-----SLNMEDEKTVVRLQEKROKELMNLKJACSKVRGPGVSGSPDSMN 677
 QY 644 KLEELSHOLLQDRAKGAQASPPPIAPYPSPTRRDLLHMQELCEGMKLLASDLDDNNR 702
 DB 678 ASRLSOPGQLMSOPSTASNS-----LPEPAKSEELVAEAAHNLIC---TLEENAIQDTYR 728

RESULT 10

US-08-890-854-2
 ; Sequence 2, Application US/08890854

Patent No. 6235512

GENERAL INFORMATION:

APPLICANT: Roche, Mike

APPLICANT: Cao, Zhaodan

TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,854
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-854-2

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Query Match 11.5%; Score 424; DB 4; Length 756;

Best Local Similarity 23.2%; Pred. No. 2e-29;

Matches 181; Conservative 123; Mismatches 325; Indels 150; Gaps 25;

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QY 9 WHTDILGOGATASYKARKKSGELVAVKFNTSYLRPREVQREFEVLRLKLNHONIV 68
DB 15 WEKMRRLTGCGVNIWMHNOETGEQIAIKOCROELSPRNNRWCLEIQIMRLTHPNV 74
QY 69 KLFAYEE---TGSRQKVLVMEYSSSLSVLESPENARGLEPDEFLVLRGVAGMN 124
DB 75 AARDVPEGMQNLAPNDLPILAMEYCOGGDLRKRYLNQFENCCGLRGALITLSDIASALR 134
QY 125 HIRENGIVHRDIKPGINIRLVGEESQSYKLTDFGARELDDEKFEVSVGTEEYIHPDM 184
DB 135 YLHERRIIRHDLKPNINYLQOGEQ-RLIHKTIIDLGAKELDOGSICTSFVGTIQLAPEL 193
QY 185 YERAVLRKPOKAGFYVDLMSIGVTLVHAATGSLPPIFGGP-----RRNKEIMYRI 237
DB 194 LE-----OQKTYIVTDYMSFGTLAEFCITGRPRPLPNQPVQWMSKYKQKSEVDIV 245
QY 238 TTERPAGIAGQRRNGPLMSYTLPTQSLGQSOLVPLANTLLEVDQAR-----C 292
DB 246 SEDL-----NOTVAFSSSLPRPNMLNVLARLEKWLQIMLMHMPRGRTDPT 293
QY 293 WGFQOFATISDILQRYVAVFESLSQAVLHHIYTHAHTIAIFQEAHKOVSAPRHQY 352
DB 294 YGPNCGCKRALDDILNLKLVHILNMTGTIHTYPTVEDESLOSILKARIQODTGIPEEDQL 353
QY 353 LFEHGLVLEPVSVAOHIA-----HTTASSPLTLFSTA-----IPKGLA-- 391
DB 354 LQAGLALIPDKPATOCISDGKLNHGTLMMDLVFLPDSKITYETQISRPPOESVSCI 413
QY 392 FRPDALVPKF-VPK-----DLQADYNTAKVLAGAGYQALRLARALLDGOELMR 441
DB 414 LQEFKRLIAEFOLKRVGWGOWHSTQTLKEDCNRLQ-----QOQRAAMNLLRNNSCLS 466
QY 442 GLHVMVEVLATGCRTELEVARTSLIYSSSLGTERSS-----SVAGTPET--QELKAA 493
DB 467 KKNMSMASQOULKAKIDFKETSI-----QIDLEKYSQETEFITSDKILLAWREMOAV 521
QY 494 ELRSR---LRTLAELVSRCSQNTITEQES-----LSSLARELV-----KSRD 533
DB 522 ELGGRREVEVLIRRMALOTDVIDLQSRPMGKOGGTLDLEEQARLEYRLRLREKPRDQ 581
QY 534 VHEDRS-----IQIQCCLDMNFTYKQFKSRMRPGIAGYNEQIHKLDKYNFSLHAK 586
DB 582 RTGDSQSEWVRLILQAIQSPEKIVAVIYIQTLSKT-----VCKOKALELLPKV----- 629
QY 587 RLQVQOEVEYQKASLYTHGRKRVYHETRNHRLVGCSSVAACNT---EAGVQVESIS 643

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DB 630 -----EEVY-----SLMNEDEKTVLRLOEKROKELMNLKIACSKVRGPGSGSPDSMN 677
QY 644 KILEELSHQLLODRAKGAQAASPPPIAPYSPTRRDLILHMOELCEGMKILASDLDDNNR 702
DB 678 ASRLSQPOLMSOPSTASNS-----LPEPAKXSEIVAEAHNLC---TLENAIOTIVR 728

```

RESULT 11

US-09-023-324-2

Sequence 2, Application US/09023324

Patent No. 6235513

GENERAL INFORMATION:

APPLICANT: Rothe, Mike

APPLICANT: Cao, Zhaoan

TITLE OF INVENTION: IKK- γ Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,324

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/890,854

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-006-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 756 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-023-324-2

Query Match 11.5%; Score 424; DB 4; Length 756;

Best Local Similarity 23.2%; Pred. No. 2e-29;

Matches 181; Conservative 123; Mismatches 325; Indels 150; Gaps 25;

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QY 9 WHTDILGOGATASYKARKKSGELVAVKFNTSYLRPREVQREFEVLRLKLNHONIV 68
DB 15 WEKMRRLTGCGVNIWMHNOETGEQIAIKOCROELSPRNNRWCLEIQIMRLTHPNV 74
QY 69 KLFAYEE---TGSRQKVLVMEYSSSLSVLESPENARGLEPDEFLVLRGVAGMN 124
DB 75 AARDVPEGMQNLAPNDLPILAMEYCOGGDLRKRYLNQFENCCGLRGALITLSDIASALR 134
QY 125 HIRENGIVHRDIKPGINIRLVGEESQSYKLTDFGARELDDEKFEVSVGTEEYIHPDM 184
DB 135 YLHERRIIRHDLKPNINYLQOGEQ-RLIHKTIIDLGAKELDOGSICTSFVGTIQLAPEL 193
QY 185 YERAVLRKPOKAGFYVDLMSIGVTLVHAATGSLPPIFGGP-----RRNKEIMYRI 237
DB 194 LE-----OQKTYIVTDYMSFGTLAEFCITGRPRPLPNQPVQWMSKYKQKSEVDIV 245

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QY 238 TTEKPGATAGARRENGBLEMSYTLPTICSLGLOSLVPLIANILEVQAK-----C 292
DB 246 SEDL-----NGTVKFSSSLPYNNLNLSVAERLEKWLQMLMHPROGCTDPT 293
QY 293 WGFDOFAETSDILOVVVHVFSLSQAVLHNYIHANHTIAFOEAVHKOTSVAERHOEY 352
DB 294 YGPNCGFKALDDILNKLVLHLMVGTIHTYVTEDESLOSUKARIQODTGIPREDEL 353
QY 353 LPEGHLCVLEPSVAOHA-----HTTASSPLLFSTA-----IPKGLA-- 391
DB 354 LOEAGIALIPDKPATQCSIDGKLINEGHTLMDLVLEFDSKITYETQISPRQPEVSOCI 413
QY 392 FRDPALDVPEF--VPKV-----DLQADYNPAKGVLAGYQALRLARALDGOELMR 441
DB 414 LOEPKRNLAFFOLRKWGVVHISITLKEDCNRLQ-----OGORAAAMNLLRNNSCLS 466
QY 442 GLHVMVEVLOATCRRTLEAVARTSLYSSSLGTERFS-----SVAGTPEI--OELKAA 493
DB 467 KMKNSMAMSQOLKAKLDFPKTSI-----QIDLEKXSEQTEFGITSCLKLLAMREMOAV 521
QY 494 ELRSR---LRTLAEVLSRCSQNTTEOES-----LSLNRELV-----KSRO 533
DB 522 ELGRENENEKLLVERMALOTDVLQDRSPMGKOGGTLDDLEOARELYRLREKPRD 561
QY 534 VHEDRS-----IQOICCLDKMNFYKQFKSRMRPGIGYNEOIHKIDKYNFSLAK 586
DB 582 RTEGDSQEMWRLLOAIQSEKRVYITQLSKT-----VCKOKKALELPKV----- 629
QY 587 RLQVFOECVQKYQASLVTHGKRMRVHETRNHLRLVGCVAACNT---EAQOVESLS 643
DB 630 -----EEVY-----SLNMEDEKTVRLQEKROKELMNLKJACSKVGPVSGSPDSMN 677
QY 644 KLEELSHOLLQDRAGAOASPPPIAPYSPTRKDLLHMOELCEGMKLLASDLLDNR 702
DB 678 ASRLSOPQGLMSOPSTASNS-----LPEPAKSEELVAEHNLC---TLEHAIQDTVR 728

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RESULT 12
US-09-168-629-15
; Sequence 15, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
; APPLICANT: Karin, Michael
; APPLICANT: D'Donato, Joseph A.
; APPLICANT: Rochawarf, David M.
; APPLICANT: Hayakawa, Makio
; APPLICANT: zandi, Ebrahim
; TITLE OF INVENTION: Ikb Kinase, Subunits Thereof, and Methods of Using Same
; FILE REFERENCE: P-UD 3295
; CURRENT APPLICATION NUMBER: US/09/168, 629
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061, 470
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-168-629-15

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Query Match 11.5%; Score 424; DB 4; Length 756;
Best Local Similarity 23.2%; Pred. No. 2e-29;
Matches 181; Conservative 123; Mismatches 325; Indels 150; Gaps 25;

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QY 9 WHTDDLQGGATASYKRNKSGELVAVKVFNTSYLRPREVQVREFEVLRKLNHOIY 68
DB 15 WEMERLGTGGFNVIRHNOETEQIALKOCROELSPRNERMCLQIMKRLTHPVV 74
QY 69 KLFVAVE-----TGSROKVLVMEYCSSLVLESPENAGLPEDFLVLRGVACNM 124
DB 75 AARVPEGMQNLAPNDPLFLAMEYCOGGDLARKYNQFENCGGLRNGAILTLTLLSDIASLR 134

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QY 125 HLRNGIVHRDIPKGNIRLVGEGOSIYKLTDFGARELDDDEKFSVYGTEEYLRPDM 184
DB 135 YLHNRITIRHDLKPRNIVLQOGEQ--RLHKITDLOAYANELQOSICTSFVGTQYLAEL 193
QY 185 YERAVLRKROKAFGVTVDLMSIGVTLHYAATGSLPFIPEGP-----RNKEIMYRI 237
DB 194 LE-----QOKYTVYDVWSFGTLAEECTIGFPPFLPNMQPVOMHSKVRKSEVDIV 245
QY 238 TTEKPGATAGARRENGBLEMSYTLPTICSLGLOSLVPLIANILEVQAK-----C 292
DB 246 SEDL-----NGTVKFSSSLPYNNLNLSVAERLEKWLQMLMHPROGCTDPT 293
QY 293 WGFDOFAETSDILOVVVHVFSLSQAVLHNYIHANHTIAFOEAVHKOTSVAERHOEY 352
DB 294 YGPNCGFKALDDILNKLVLHLMVGTIHTYVTEDESLOSUKARIQODTGIPREDEL 353
QY 353 LPEGHLCVLEPSVAOHA-----HTTASSPLLFSTA-----IPKGLA-- 391
DB 354 LOEAGIALIPDKPATQCSIDGKLINEGHTLMDLVLEFDSKITYETQISPRQPEVSOCI 413
QY 392 FRDPALDVPEF--VPKV-----DLQADYNPAKGVLAGYQALRLARALDGOELMR 441
DB 414 LOEPKRNLAFFOLRKWGVVHISITLKEDCNRLQ-----OGORAAAMNLLRNNSCLS 466
QY 442 GLHVMVEVLOATCRRTLEAVARTSLYSSSLGTERFS-----SVAGTPEI--OELKAA 493
DB 467 KMKNSMAMSQOLKAKLDFPKTSI-----QIDLEKXSEQTEFGITSCLKLLAMREMOAV 521
QY 494 ELRSR---LRTLAEVLSRCSQNTTEOES-----LSLNRELV-----KSRO 533
DB 522 ELGRENENEKLLVERMALOTDVLQDRSPMGKOGGTLDDLEOARELYRLREKPRD 561
QY 534 VHEDRS-----IQOICCLDKMNFYKQFKSRMRPGIGYNEOIHKIDKYNFSLAK 586
DB 582 RTEGDSQEMWRLLOAIQSEKRVYITQLSKT-----VCKOKKALELPKV----- 629
QY 587 RLQVFOECVQKYQASLVTHGKRMRVHETRNHLRLVGCVAACNT---EAQOVESLS 643
DB 630 -----EEVY-----SLNMEDEKTVRLQEKROKELMNLKJACSKVGPVSGSPDSMN 677
QY 644 KLEELSHOLLQDRAGAOASPPPIAPYSPTRKDLLHMOELCEGMKLLASDLLDNR 702
DB 678 ASRLSOPQGLMSOPSTASNS-----LPEPAKSEELVAEHNLC---TLEHAIQDTVR 728

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RESULT 13
US-08-910-820-9
; Sequence 9, Application US/08910820
; Patent No. 6258579
; GENERAL INFORMATION:
; APPLICANT: Mercutio, Frank
; APPLICANT: Zhu, Henry I.
; APPLICANT: Barbosa, Miguel
; APPLICANT: Li, Gian
; APPLICANT: Murray, Brian W.
; TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
; TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910, 820

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FILING DATE: 12-AUG-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MAKI, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 860098.413C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 756 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-910-820-9

Query Match 11.5%; Score 424; DB 4; Length 756;
 Best Local Similarity 23.2%; Pred. No. 2e-29;
 Matches 181; Conservative 123; Mismatches 325; Indels 150; Gaps 25;

QY 9 WHTDLLGAGATASYKARKKSGELVAVKVFNTSYLRPREVOYREFEVLRLKLNONTIV 68
 DB 15 WEKRELGIGGFGVYIRHINOTGEOIAIKOCROELSPRRRCWCLEIQIMRHLHPNVY 74
 QY 69 KLFAYBE---TGSROKVLVMEYCSSGSLVLESPENAFGLPDEFLVLRVAVAGNN 124
 DB 75 AARDVEGMONLAPNDLPLAMEYCOCGDLRKYLNOFENCGSLRNGALITLSDIASALR 134
 QY 125 HIRENGIVHRDIKPGNIMLVEEGOSIYKILDFENARELDDDEFVSYGTEYLHPDM 184
 DB 135 YLHNRITIRDLKRPENIVLOOGEQ-RLHKIIDLGAARELDGSLCTSPVGLQYLADEL 193
 QY 185 YERAVLRPRQKAFGVTVDLMSIGVTLVHAATGSLPFIIPFGP-----PRNKRIYRI 237
 DB 194 LE-----QQKYTVVDYMSFGTIAFECTIGFRPFLPNMQPVGMHSHVAKQKSVDIVV 245
 QY 238 TEKPAGAIAGQRENGPLEMSTYLPITTCQLSLGLOSLVPIIANILEVBOAK-----C 292
 DB 246 SDDL-----NCTVRFSSSLPYPNNLNSYLAEIRLKWLOLMWMPHROGTDPT 293
 QY 293 WGFDOFAETSDILQRVVHVFSLSQAVLHHIYIHAHTIAIFQAVYKOTSVAPRHOEX 352
 DB 294 YGNCCFKAADDILNLKILHNMVTGITHYPTVEDESLSIKARIQODTGIPEDDEL 353
 QY 353 LFEGLHCVLEPVSQAQHA-----HTTASSPLTFESTA-----IPKGLA-- 391
 DB 354 LOEAGLALIPDKPATOCISDGLKNEGHTLMDIVLEFDNSKITETQISPRAPQESVSCI 413
 QY 392 FRPDALDVPKF-VPKV-----DLQADVNTAKGVLAGYQALRLARALLDGOELMFR 441
 DB 414 LOEPKRNIAFHLKRVQWGVHSTQTLKEPCNRLQ-----OGORAMNMLNNNSCLS 466
 QY 442 GIHWMEVLAOTCRTELEVARTSLYSSLSGTERFS-----SVAGTPEI--OELKAA 493
 DB 467 KMKMSMASMSQOLKAKIDPFKTSI-----QIDLEKYSBOQTEFGITSDKLLAMREMOAY 521
 QY 494 ELRSR---LRTLAELVNSGSONITEQES-----LSLNRELV-----KSRDQ 533
 DB 522 ELGCRNEBVKLLVERMALQTDIVDQSPGRKOGGTLDDLEQARELYRLREKPRDQ 581
 QY 534 VHEDRS-----IQOIOCCLDKMNFIYKOPKSRMRPGSGYNEOJHKLDKYVNSHLAK 586
 DB 582 RTEGDSQEMVRLLOALQOSPEKAVITYTQLSKT-----VYCKOKALELLPKV----- 639
 QY 587 RLLOVFOBEVYQKQASLVTHGKRMRYVHETRNHLRLVGSVAACNT---EAQVOESLS 643
 DB 630 -----EEVY-----SLNMEDEKTVVRLQEKROKELMNLKLTAKSVVRPVGSDPSMN 677
 QY 644 KLEBELSHOLLQDRAKQAQASPPRIAPYPSPTKRDILLHMOELCEGKLLASLDLNNR 702
 DB 678 ASRLSOGQLMSOPSTIASNS-----LPEPAKSEELVAEAAHNC---TLLENAIQDITVR 728

RESULT 14
 US-08-887-518-3
 ; Sequence 3, Application US/08887518
 ; Patent No. 5843721
 ; GENERAL INFORMATION:
 ; APPLICANT: Rothe, Mike
 ; APPLICANT: Wu, Lin
 ; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/887,518
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: T97-008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 745 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-887-518-3

Query Match 10.7%; Score 394; DB 2; Length 745;
 Best Local Similarity 23.0%; Pred. No. 9.9e-27;
 Matches 161; Conservative 116; Mismatches 300; Indels 122; Gaps 24;

QY 9 WHTDLLGAGATASYKARKKSGELVAVKVFNTSYLRPREVOYREFEVLRLKLNONTIV 68
 DB 15 WEKRELGIGGFGVYIRHINOTGEOIAIKOCROELSPRRRCWCLEIQIMRHLHPNVY 74
 QY 69 KLFAYBE---TGSROKVLVMEYCSSGSLVLESPENAFGLPDEFLVLRVAVAGNN 125
 DB 75 KACDVEBELNLIHNDVPLAMEYCSGDLRLKLNKRENCCKGKESQILSLDISGIRY 134
 QY 126 IRENGIVHRDIKPGNIMRLVGEEOISYKILDFENARELDDDEFVSYGTEYLHPDMY 185
 DB 135 YLHNRITIRDLKRPENIVLOOGEQ-RLHKIIDLGAARELDGSLCTSPVGLQYLADEL 193
 QY 186 ERVAVLRPRQKAFGVTVDLMSIGVTLVHAATGSLPFI-----PFGGPRNRKELMYRITTEK 241
 DB 194 E-----NKPYTAVDWSFCTWFEICAGYRFLNHLQPFVWHEKIK-----KK 237
 QY 242 PAGAIAGQRENGPLEMSTYLPITTCQLSLGLOSLVPIIANILEVBOAK-----C 292
 DB 238 TEKPAGAIAGQRENGPLEMSTYLPITTCQLSLGLOSLVPIIANILEVBOAK-----C 292
 QY 289 QAKCWGFDFAETSDILQRVVHVFSLSQAVLHHIYIHAHTIAIFQAVYKOTSVAPR 348
 DB 297 QPRC-----FVLMDBHILNLKILHNMVTGITHYPTVEDESLSIKARIQODTGIPEDDEL 350
 QY 349 HOEYLFEGHL-----CVLEP-----SVSAQHIAHTTASSPLTFESTAIPKGLA 391

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Db 351 SQELLSETGISLDPKRPASQCVLDGVRGCDSTWVILFEDKSKTYVEGPAASRSLSDCVNT 410
QY 392 FDPALDVPKF-VPKV-----DLQADYNTAKVGLAGYQALRLARALLDGOELMFR 441
Db 411 VODSKTQLPTIOLRKVMAEAVHYVSGLKEDYSRL-----FQGRAMLSTL-----LRYN 459
QY 442 GLHWMEVLOATCRRTLEVAFTSLYLSSLGTERPSS--VAGTPEIOLKAAELRSRL 499
Db 460 ANLTMMKNTLISASOOLK-AKLEFFPKSIOLDLERYSEOMTYGISSEKMLKAMEEKA 518
QY 500 RTLAEVLSRCSQNTETQESLSLNRELKVSQDVHEDRSIQOCCLDKMFITYKQFK 559
Db 519 IHXAEV-----GVIGYLEDQIMSLAEIMELQKSPYGRQGDLMESLHQRALIDYQLKH 573
QY 560 SMRPG-LGYNEQ-----IHKLD-----KVNFSHLAKRL-----LOVFOE 594
Db 574 ---RPSDHSYSDSTEMVKIIVHTVQSDRYLKERFGLSKLGCOKIIDLPRKEVALS 630
QY 595 ECVQKYQASLVTHGKRMVHETRNHLRLVGCSSVAACNT 633
Db 631 NIKEDNTVMFMQGRKKEIW---HLKIACQSSARS 665

RESULT 15
US-09-023-321-3
: Sequence 3, Application us/09023321
: Patent No. 5844073
: GENERAL INFORMATION:
: APPLICANT: Roche, Mike
: APPLICANT: Wu, Lin
: TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 268 BUSH STREET, SUITE 3200
: CITY: SAN FRANCISCO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/023,321
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/87,518
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: T97-008
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 745 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-023-321-3

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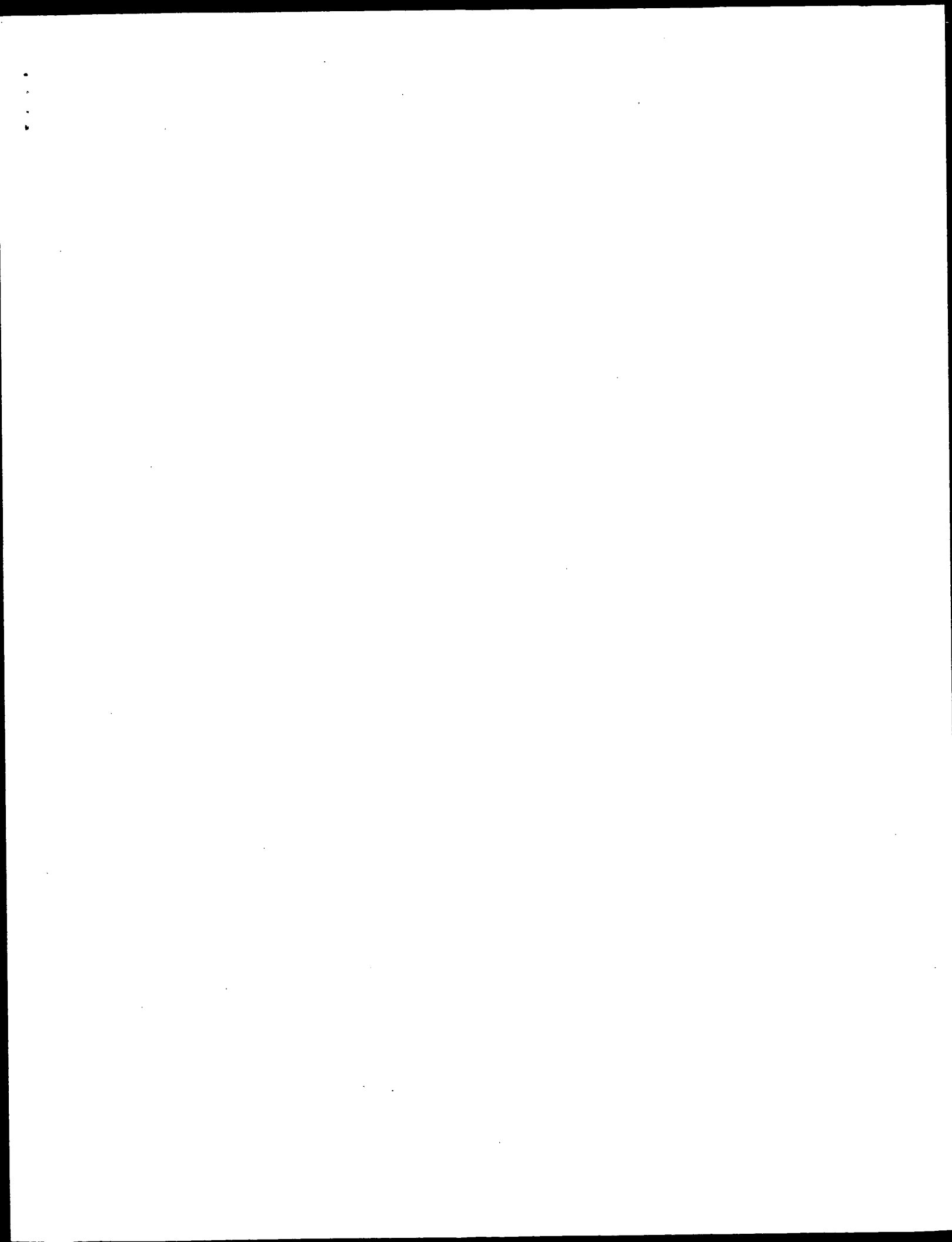
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QY 9 WHITDILGOGATASVYKARKNKKSGELVAVKYFNNTSYLRPREVOVREFEVLRKLNHONTV 68
Db 15 MEMRELTGTGGVNCVLYOHRELDTKAIKSCRELSTKNEBRMCHELOIKKKLNHNVT 74
QY 69 KLFVEETGG---SRQKLVMEYCCSSGSLSVLSEPNAPFLPEDEFIVLRGVAGMNH 125
Db 75 KACDPEELNILLIHDPVPLAMEYCSGGDLRLKLNKPECCCLKESQILSLSDIGSGIRY 134
QY 126 LRENCIVHDIKPCGNIMLVBEQSGSYKLLTDFCAARELDDEKFEVSYGTEEYLRHPMY 185
Db 135 LHENKTIHRDLKPEYIV-LQDVGKRIHKIIDLGYAKDDVQSGSLCTSFVGTLYLAELF 193
QY 186 ERAVLKRPQKAFQVTVDLMSIGVLYHAATGSLPEI---PFGSPRNKEIYRITTEK 241
Db 194 E-----NKPYATVDYNSFGTMVEPCIAGYRPLHHILOPFYWHKIR-----KK 237
QY 242 PAGIAGAQRENGPLEWSTLP---ITCOLSLGASOLVPIIAN-----ILEVE 288
Db 238 DPKCIFACEEM-SGEVRFSSHLPPQNSLSLIVEPMENWLOLMNMPQGRGVPDLTK 296
QY 289 QAKCMGFQDFFAETSDILQRVVHVFEISQAVLHHIYTHAHNTAIFQEAHVHKQTSVAPR 348
Db 297 QPRC-----FVLMDHILNLKIYHILNMTSAKIIISPLLPDESLSHSQSIHERETGINTG 350
QY 349 HOEYLFEGHL-----CVLEP-----SVSAQHIAHTTASSPLTLESTAIKGLA 391
Db 351 SQELLSETGISLDPKRPASQCVLDGVRGCDSTWVILFEDKSKTYVEGPAASRSLSDCVNT 410
QY 392 FDPALDVPKF-VPKV-----DLQADYNTAKVGLAGYQALRLARALLDGOELMFR 441
Db 411 VODSKTQLPTIOLRKVMAEAVHYVSGLKEDYSRL-----FQGRAMLSTL-----LRYN 459
QY 442 GLHWMEVLOATCRRTLEVAFTSLYLSSLGTERPSS--VAGTPEIOLKAAELRSRL 499
Db 460 ANLTMMKNTLISASOOLK-AKLEFFPKSIOLDLERYSEOMTYGISSEKMLKAMEEKA 518
QY 500 RTLAEVLSRCSQNTETQESLSLNRELKVSQDVHEDRSIQOCCLDKMFITYKQFK 559
Db 519 IHXAEV-----GVIGYLEDQIMSLAEIMELQKSPYGRQGDLMESLHQRALIDYQLKH 573
QY 560 SMRPG-LGYNEQ-----IHKLD-----KVNFSHLAKRL-----LOVFOE 594
Db 574 ---RPSDHSYSDSTEMVKIIVHTVQSDRYLKERFGLSKLGCOKIIDLPRKEVALS 630
QY 595 ECVQKYQASLVTHGKRMVHETRNHLRLVGCSSVAACNT 633
Db 631 NIKEDNTVMFMQGRKKEIW---HLKIACQSSARS 665

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Search completed: May 14, 2002, 19:11:28
Job time: 5875 sec

Query Match 10.7%; Score 394; DB 2; Length 745;
Best Local Similarity 23.0%; Pred. No. 9, 9e-27;
Matches 161; Conservative 116; Mismatches 300; Indels 122; Gaps 24;



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: May 14, 2002, 19:00:08 ; Search time 76.26 Seconds
(without adjustments)

Title: US-09-582-397A-2

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Perfect score: 30/4
Sequence: 1 MGTANYLMHTDILGGAT.....LDNNRIIERLNRPAPPDV 716

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 08

Database : PIR_71:★

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1: plr1: *
2: plr2: *
3: plr3: *
4: plr4: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	399.5	10.9	745	1	149101	conserved helix-1d
2	305.5	8.3	1051	1	JM0051	serine/threonine-s-
3	293	8.0	1097	2	P96538	hypothetical protea
4	291	7.9	1006	2	T26770	hypothetical prote
5	286.5	7.8	713	2	S27966	probable serine/thr
6	286.5	7.8	1142	2	S59359	G1N4 protein - yea
7	285.5	7.8	863	2	C68856	protein R107.4 lim
8	282.5	7.7	795	2	S30874	hypothetical protei
9	281	7.6	480	2	S56639	ribosomal protein
10	281	7.6	897	2	S61137	probable membrane
11	276	7.5	821	1	A39616	protein kinase RAD
12	276	7.5	915	2	S74283	probable protein k
13	274	7.5	1231	2	T18532	serine/threonine p
14	273.5	7.4	706	2	A48084	SWI1 protein kinase
15	272.5	7.4	836	2	B96716	probable serine/thr
16	269.5	7.3	556	2	T42100	serine/threonine f
17	266.5	7.3	556	2	T36502	serine/threonine f
18	266.5	7.3	745	2	G01025	serine/threonine f
19	266.5	7.3	756	2	T50298	MAP kinase kinase
20	266.5	7.3	918	1	I48719	protein kinase C
21	266	7.2	348	2	T37321	Ca2+/calmodulin-d
22	266	7.2	445	2	T43420	probable protein
23	266	7.2	733	2	A57459	ribosomal protein
24	265.5	7.2	465	2	S68462	protein kinase Atp
25	265.5	7.2	542	2	T08777	probable protein
26	265	7.2	735	2	I51901	ribosomal protein
27	264	7.2	1062	2	S46367	protein kinase CD
28	264	7.2	1192	2	T18611	probable serine/thr
29	264	7.2	1246	2	G89287	protein H39E23.1

30	263.5	7.2	471	2	S68463	protein kinase ATR
31	263.5	7.2	774	2	I48609	probable serine/thr
32	263.5	7.2	912	1	A53215	protein kinase C (
33	263	7.2	733	1	B30001	ribosomal protein
34	262.5	7.1	658	2	S39500	serine/threonine-s-
35	262	7.1	856	2	T43631	serine/threonine k
36	262	7.1	1142	2	S50632	protein kinase PAM
37	261.5	7.1	560	2	T14616	hypothetical prote
38	261	7.1	629	2	A43001	ribosomal protein
39	261	7.1	1233	2	T14157	serine/threonine p
40	260	7.1	735	2	A53300	ribosomal protein
41	260	7.1	740	2	T24340	hypothetical protei
42	260	7.1	797	2	T23827	hypothetical prote
43	260	7.1	1314	2	S19488	probable membrane
44	257.5	7.0	2783	2	T34416	hypothetical prot
45	256	7.0	752	1	A32571	ribosomal protein

ALIGNMENTS

QY	149101	conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse
Db	C:Species: Mus musculus (house mouse)	
QY	C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999	
Db	C:Accession: 149101	
QY	C:Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.	
Db	C:Genomics 27, 348-351, 1995	
QY	A:Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome	
Db	A:Reference number: 149101; MUID:96044444	
QY	A:Accession: 149101	
Db	A:Status: Preliminary; translated from GR/EMBL/DBJ	
QY	A:Molecule type: mRNA	
Db	A:Residues: 1-745 <RES>	
QY	A:Cross-references: EMBL:U12473; NID:g1079492; PID:AMC52589.1; PID:g1079493	
Db	C:Genetics:	
QY	A:Gene: CHUK	
Db	C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase hom	
QY	C:Keywords: ATP; phosphotransferase	
Db	F:13-283/Domain: protein kinase homology <KIN>	
QY	Query Match	
Db	Best Local Similarity 22.8%; Pred. No.1,1e-11;	
QY	Matches 175; Conservative 118; Mismatches 283; Indels 193; Gaps 28;	
QY	9 WHTDDLGGATASVYKARKKSGELVAVKVFNTTSYLRPREVQVREVEYLRKLHNOIV 68	
Db	15 WEMRERLTGGFGVNSLYQHRELDKIAIKSORLELSENNRMCHEIOIMKKIDHANV 74	
QY	69 KLFAYEETGG---SQKYLVMETGSSGSLSTVLESPENFAGPDEDFVLVLCVAGMNH 125	
Db	75 KACDVPPEELNLTINDVPLAMEYCSGGDLRKILNKPENCCKGKEQILSLSDISSGIRY 134	
QY	126 LRENGIVHNDIKPQINIMRLVGEOSIYKLTDFGAARELDDEKTVSYVGYEELVHPDMY 185	
Db	135 LHNKTIHRDLDPENIV-LQDVGGKTIHKIIDVYAKVDQGSCLTSPFGTLQYLAPELF 193	
QY	186 ERAVLAKKPOOKAFGVYVDLMSGVTLYHAATGSLPI---PFGGRRKKEIMRTTTER 241	
Db	194 E-----NKRYTAVDVWDSFGTWFECSIAGRPRLHLLDPTTWHEKIR-----RK 237	
QY	242 PAGAIAGAOORENGPTEMSYTLR---ITCOLSLGLOSQVLPILAN-----ILVEE 288	
Db	238 DKRCITACEEM-TGEVRFESHLPQPNLSCLSLIVERPESWLOQLMNDPQOGRGPDITLTK 296	
QY	289 QAKCWGEQDFFAETSDILQVVVHVFSLSQAVLHHIYIHAHNTIAIQEAVHKQTSVAPR 348	
Db	297 QPRC-----FALMDIILNLTIVHILNMTSAKIISFLPCDSSLQSRIRIEGTINTG 350	
QY	349 HQYLFEGHLCVLEPVSVAQHIAHTTASSPLTLFSAIPKGLAFRPPALDVFKEFVQVDL 408	

Db 351 SOELLSETGIS-LDP-----RKPA----- 368

Qy 409 QADYNTAGVLAGAGYOLRLARALIDGQELMFGIHWMEVIAQACRTE---VARTSL 465

Db 369 -----SQCVIDG-----VRGCDSTMYVLFPDKSKIVYGPAPSRS-- 402

Qy 466 LYLSSLSCTERRSSVAGPEIQLKAAELRSRLTAEVLSRCSQ----- 511

Db 403 --LSDCVNYIVODSKIQIPIILKRVMAEAVHYVSGLEKEDYSRLFCGGRAMLILRYNA 460

Qy 512 NITTEQESLSINREL-----VKSRODVHEDRSIQIQOCL--DKMFIYKQKRSRM 563

Db 461 NLTKMKNLISASQDLAKLFFPKRSIQDLERTSEQMTGTSSEKMKAKWEMEKAH 520

Qy 564 PG---LGYNEEQ-----IHKLDKVFNSHAKRLLOVEQECVQKYO----- 601

Db 521 YSEVGVGLTDDQIMSLTETMELOKSPYGRQGLDMESLEGRALIDLYKQKHPDHL 580

Qy 602 -----ASLYTH--GKRVRVYHETRNH--RLVGC-----SYAACN-TEAG-VQ 639

Db 581 SDSTEMKVIIVYVOSQDRVLKELFGHLSKLLGCKOKIIDLPRVEVALSNKEADNTVM 640

Qy 640 ESLSKLEELSHOL-----LQDRAKGAQAS-----PPIAPYSPPTPKD 678

Db 641 FMQGRKQKEIWHILKIACTQSSANSIVGSSLEGTVPYPPVAMLPPTLAD 689

RESULT 2

JM0051
serine/threonine-specific protein kinase (EC 2.7.1.1) ULK1 - mouse
N:Alternate names: protein kinase UNC-51-like
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JM0051
R:Van, J.; Kuroyanagi, H.; Kuroiwa, A.; Matsuda, Y.; Tokumitsu, H.; Tomoda, T.; Shirasawa, Biochem. Biophys. Res. Commun. 246, 222-227, 1998
A:Title: Identification of mouse ULK1, a novel protein kinase structurally related to C.
A:Reference number: JM0051, MVID:98262945
A:Accession: JM0051
A:Molecule type: mRNA
A:Residues: 11051 <YAN>
A:Cross-references: GB:AF053756; NID:93136153; PIDN:AAC40118.1; PID:93136154
C:Genetics:
A:Map position: 12q16.3
C:Superfamily: mouse protein kinase ULK1; protein kinase homology
C:Keywords: phosphotransferase
F:14-278/Domain: protein kinase homology <KIN>

Query Match 8.3%; Score 305.5; DB 1; Length 1051;
Best Local Similarity 26.8%; Pred. No. 3.8e-07;
Matches 91; Conservative 52; Mismatches 127; Indels 69; Gaps 10;

Qy 1 MOSTAWYIMHTDILGOGATASYKARKNKSGEL-VAVKVENTSYLRPREVOVREFEVL 59

Db 8 VETVGKFEFSRKLIGHGFAVYFKGRHREKHDLVAVKCNKKNLAKSQTLGKIKIL 67

Qy 60 RKLHNOHYVLFVVEETGSRQKVLMEYCGSSGLSVLESPNAGLEDEDEIVLVLRV 119

Db 68 KELKHENIVALYDFQEMANS--YVLMEYCGNGDLADYHTMKT--LSEIVRLFLQOI 122

Qy 120 VAGMNLRENGIVHDIKFGNIMRLVGEQSI-----YKLTDFGARELDDDEKFAV 173

Db 123 AGAMRLIHSIGLIIHDLKPNIL--LSNPGRRANPSINIVKILADGFAVYLOSNNMAATL 181

Qy 174 YGTEVYLHDMYERAVLKRPOKAEVYVDMSIGVTLVHAATGSLPTFGSPRRNKI 233

Db 182 CGSEPMIAAEVIT-----MSQHYDGKADLWSIGIVYQCLTGKAPF-----QASSPQ 227

Qy 234 MYRTTEKPAAGIAGAQRRENGPLEMSYTLPTCOLSIGISQOIVPIIANLIEVDAQCW 293

Db 228 DLRLFEKKKTIIVPAIPRETSAPLR-----QLLLAL-----LQNRHKKDM 267

Qy 294 GDOEFAETSDIILQRRVYVHFSLSQAVLHITYHANNTI 332

Db 268 DFDEFF-----HHPFLDASTPI 284

RESULT 3

P96538
hypothetical protein F1413.15 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96538
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hughes, M.R.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marzla, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MVID:21016719
A:Accession: F96538
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1097 <STO>
A:Cross-references: GB:AE005173; NID:95734778; PIDN:AAD50043.1; GSPDB:GN00141
C:Genetics:
A:Gene: F1413.15
A:Map position: 1

Query Match 8.0%; Score 293; DB 2; Length 1097;
Best Local Similarity 33.3%; Pred. No. 1.5e-06;
Matches 72; Conservative 50; Mismatches 72; Indels 22; Gaps 9;

Qy 9 WHITDILGOGATASYKARKNKSGELVAVKVENTSYLRPREVOV--REFEVLKRLNHN 66

Db 6 YHIELVGEBSFGRYVKGRRKYTGOTVAMK-FIMQGTDKDHSILREIELKRLKEN 64

Qy 67 IYKLFVVEETGSRQKVLMEYCGSSGLSVLESPNAGLEDEDEIVLVLRVAGMNL 126

Db 65 ILEM-LDSFENAREFCVYTFE-AQGELEFIEDDK---CLPEEQVQAIQAQVVALDYL 118

Qy 127 RENGIVHDIKFGNIMRLVGEQSIYKLTDFGARELDDDEKFPV-SYVGTEVYLHDMY 185

Db 119 HSNRIIHRDMKPNIL--LIG--AGSVVAKLCPDFGFRKAMSTNTVYLRKSTGTPYMAPELV 174

Qy 186 ERAVLRKPOKAEVYVDMSIGVTLVHAATGSLPF 221

Db 175 -----KEOPYDRTVDLWSIGVILYELVYGOPPE 202

RESULT 4

T26770
hypothetical protein Y3968B.e - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26770
R:Smey, R.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20262
A:Accession: T26770
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1006 <MIL>
A:Cross-references: EMBL:AL110482; NID:e1542197; PIDN:CAB54389.1; CESP:Y3968B.e
A:Experimental source: Clone Y3968B
C:Genetics:
A:Gene: CESP:Y3968B.e
A:introns: 138/1; 205/3; 475/3; 713/2; 747/3; 835/2; 897/2

Query Match 7.9% Score 291; DB 2; Length 1006;
 Best Local Similarity 21.9%; Pred. No. 1.7e-06;
 Matches 167; Conservative 126; Mismatches 286; Indels 184; Gaps 37;

```

QY 7 YLWHTDLLGGQATASVYARANKSGELVAVKVF-NTSYLAREVQVEEFLAKLNLH- 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 19 YTLNDEPMKAGVSGVYRGRT-ESGRVAVKARTASAKADVAMCMEIDILKIKGV 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 QNIVKLFANEETGSGKQKLVY-----MEYSSGSLVLESPENAFGLPEDEFL-VYLR 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 78 ANIVQFGSKNTKIPGSGVETETISFAME-CASRLDAERRENRHGLPSNVLIDLVVD 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 CVVAGMNLRENGIVHHDIPGNIMRLV-----GEEGQSIYKLTDFGARELDD--EKF 170
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 137 CSMA-LSALREHNIARDIKHNNILPFGSPTRGRSTHFLKIDMGCSAISSENSQEL 195
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 VSVYGEELHPD-----MYERAVLRKPOKAFGVYVDMISIGVLYHAATGSLPFP 223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 196 NSIAGFTFLYPHIPNGHNMTKSAVYPEQ-----CDLMSIGCTLYFCATGEPFP-- 247
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 224 FGPRRKKEIMYRIT-----TEKPAQAIAGQRENG-----PLEMS-YTL 263
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 248 --ESTRADANLYHMAAVDLTRNPAAVNLVQVENPVTKERFNEPVTETELPAEFTRYPK 305
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 264 PTCQLSIGLQSLVPLILANILEVBOAKCGFPOFAETSDILQRYVYHVFSLSQAVLH 323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 306 WLYCTMTC-----LLRNFHEPST-----EYAKAVAGVARNKRRF-----ASVDQ 347
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 324 IYHANNTAIFQDPAVHKOTSVAPRHOEYLE--EGHLCVLEPSVSAQHIAHTAS---SP 378
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 348 MSIVEHDMGNILE-----SLPSISECLGPEGIDVILANTSTHYLDSKOSVDGLP 401
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 379 LTLF-----STAIPKGLAFRD-----PALDVPKVPVYDQAD- 411
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 402 DDLVLYPQTSQVEMKRLKRNKFNELBGMTDKLEIKKCYEGLSMLTEVDELID 461
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 412 YNTAKGVLAGAYOLRLARALDQELMFRGLHWMEVLAQCRRLLEVARTSLYLSS 471
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 462 FDRVSLISTFOFSL-----VQELS-----QFERVQTSFAYVYMAASPMMLFD 507
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 472 LGTRFSVAGTPETIOELKAAELRSRLR-----TLAEVLSRCSQVITTEQESTLSLR 525
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 508 EANDPAKTIADQCIQAIAKEELERHAKAMDEFACAKLSRAEDLRLEDMDLPGIRR 567
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 526 ELVSRDQVHEDRSI-----QQIQCLDKMNFYKQFKSRMRPGLYNEEQIHL 576
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 568 EI-----ESYLFYDKATILSTQKTOELVELCLKRNVTMKQIFNS---PD-GINKSKLN-- 618
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 577 DKVNFSLAKRLQVQGE-----ECVQKYQASLVTHGKRMRYVHETRN-HLRVGCSSVA 629
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 619 TAMNLAASLSQLRSDYOKLQDMISECVLLE-----KPFQYAKDMVNRVLAQOGCS-- 669
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 630 ACNTEAGVQ-----ESLSKLEELSHQLLQ 655
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 670 -RNTMKSMLLRPEFHENDIRMKSKTSCKRLDQNLKELO 711
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 5
 S27966
 Probable serine/threonine-specific protein kinase (EC 2.7.1.-) - human
 N:Alternate names: protein p78
 C:Species: Homo sapiens (man)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Mar-2000
 C:Accession: S27966
 R:Maehabwari, K.K.; Som, S.; Parsa, I.
 submitted to the EMBL Data Library, January 1992
 A:Description: Sequence of a cDNA encoding 78kd marker protein lost in chemically induce
 A:Reference number: S27966
 A:Accession: S27966
 A:Molecule type: mRNA
 A:Residues: 1-713 <MAH>
 A:Cross-references: EMBL: M80359; NID: g189511; PIDN: AA59931.1; PID: g189512
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:54-307/Domain: protein kinase homology <kin>
 F:62-70/Region: protein kinase ATP-binding motif

Query Match 7.8% Score 286.5; DB 2; Length 713;
 Best Local Similarity 23.9%; Pred. No. 1.9e-06;
 Matches 176; Conservative 91; Mismatches 283; Indels 185; Gaps 32;

```

QY 15 LGGATASVYARANKSGELVAVKVFNTSYLAREVQ--VAFEVLRKLNQNTVYKLF 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 IKGNFPAKYKLARHILTGFEVAIKIIDKQ--LNPISLQKLFREVRIMKILNPNVYKLE 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 VEETGSSRQKLVMEYSSGSLVLESPENAFG-LPEDEFLVLRVAVAGMNLRENGI 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 VIET--QKTLYLIMEYASGKVFYLY-----AHGRKKEEAKSKRQIYSAVQYCHQKRI 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 VHRDIKPGNIMRLVGEESQIYKLTDFGARELDDKFFSVYGYEEVYHLPDYERAVLR 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 175 VHRDLKAENILL-----DADMNIRIADFGFSNEFTVQCKLDTPCGSPPYAAPLPQ----- 225
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 KPOKAFGVYVDMISIGVLYHAATGSLPFIPEGPRRKKEIMYRITTEKPAQALAGAR 251
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 226 --GKKYDGEVDMVSLGVLITLVSGSLP-----DQNLKELRERY----- 265
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 252 RENGPLEMSYTLPI-----TCQLSIGLQSLVPLILANILEVBOAKW---GPDQ-----FF 299
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 266 ----LRGKTRIPFYSTDCENILKRFVLPNPKRGTLEQIMKDRINNGHEDELKRPV 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 AETSIDILQVYVHVF-----SLSQAVLHHI---YI-----HAHNT 331
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 321 EPEDLISDQKRIDIMVGMVSGOEIOESLSKMYDEITATYTLGRKSEVRPSSDLNS 380
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 332 IATFOEAVHK--QTSVAPRHOEYLFEGHLCVLEPSVA--QHTAHTASSPL----- 379
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 381 TG--QSPHKKVQNSVSSOKORNSDHAGPGIPSVAYYKRSQSTSTADSDLEKDGISRK 438
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 380 TLFSTAIPIKGLAFRDPAL-----DVPKFPYKVDLQADVYNTAKVLAGAYOLRLAR 430
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 439 STGSAVGKGIAPASPMGLNASNPNKADIFE--RKSSVPSSTATGAGMTRRTYVCSER 497
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 431 ALLDGEIMFRGLHWMEVLAQCRRTLEVART--SLYLSL-----GERS 478
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 498 TTDHRSYVIONGRE-----NSTIDPQRVASTHSISSAATPDRIIPRPGTASRS 547
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 479 SVAGTPEIOEL-----KAAELRSRLTAEVLSRCSQVITTEQESTLSLNRELYSRD 532
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 548 TFGQPRERTATYNGRPASPSLSHEATPLSOTRSRSGTTL-----FKLTSKLTLSRN 601
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 533 ----QVHEDRSIQIQCCLDKMNFYKQFKSRMRPG-----LGYNEEQI 574
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 602 VSAKQDENKEAKP-----RSLRFTWSMKTTSSMDGDMREIRKYLIDANNCDYEQREFF 656
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 575 KLDKVNFSHLAKRLQVQGEVQKYQASLVTHGKRMRYVHETRNILRLVGCSSVACNRE 634
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 657 LFCVHDGHAENLVQWEMEVCC--KLPRLSLNGVRFK-----RLSGISIAEKNT- 703
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 635 AGVQESLSKLEEL 649
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 704 -----ASKIANEL 711
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 6
 S59359
 GIN4 protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YDR507C
 C:Species: Saccharomyces cerevisiae
 C:Date: 30-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1999
 C:Accession: S59359; S69565
 R:Longline, M.S.; Pringle, J.R.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: S59359
 A:Accession: S59359

A: Molecule type: DNA
 A: Residues: 1-1142 <LON>
 A: Cross-references: EMBL:U33140; NID:9992650; PIDN:AAV5513.1; PID:9992651
 R.Dietrich, F.S.
 submitted to the EMBL Data Library, August 1995
 A: Description: The sequence of *S. cerevisiae* cosmid 8166, 9787, 9717, and lambda 3073.
 A: Reference number: S69553
 A: Accession: S69555
 A: Molecule type: DNA
 A: Residues: 1-1142 <DIE>
 A: Cross-references: EMBL:U33057; NID:9227764; PIDN:AA64949.1; PID:9227777; MIPS:YDR507C
 C: Geneticks:
 A: Gene: SGD:GIM4
 A: Cross-references: SGD:S0002915; MIPS:YDR507C
 A: Map position: 4R
 C: Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C: Keywords: ATP
 F.17-289/Domain: protein kinase homology <KIN>
 F.25-33/Region: protein kinase ATP-binding motif

Query Match 7.8%; Score 286.5; DB 2; Length 1142;
 Best Local Similarity 20.2%; Pred. No. 3.3e-06;
 Matches 181; Conservative 146; Mismatches 312; Indels 257; Gaps 40;

QY 9 WHTDDLLGOGATASYKARKKSGELVAVK-----VFN-----TTSYLRRPREV 51
 Db 19 WRLGELTIGSTGKQVQLARNGSTGQEAIVKSKAVFTGNGVSGTSIVGSTTPDAPLPGI 78
 QY 52 QVREVEVLRLKLNHONIVKLFVAEEFGSGROKLVMEYSSGSLISVL--ESPENAFGLPE 109
 Db 79 E-RETIKLNHNPVNLVDYWER--NTDLVILEYAEKEBELFNLLVERGP-----LPE 130
 QY 110 DEFLVVLACVAGMHLRENGIVHRDIKPGNIMLVGEGGSIYKLTDFGAARELDDDEK 169
 Db 131 HEAIFEFQIIGVSYCHALGIYHRDLKPEMLL---DHKYNIKIADFGMAALETECKL 186
 QY 170 FVSVYGTGEYLHPDKYERAVLRKPKQKAFGYVDLMSIGVLLYNAAGTSLEFFIRGG--- 226
 Db 187 LETSGSGHYAPAEI---VSGIPQ---GRASDWSGCVILFALLTGRLPDEEDGIR 239
 QY 227 -----PRNKEMIRITTEKPA-----GALGAQ 250
 Db 240 TLLLVKGGEFEMPSDEDEISREADLRKILTVPERIKTRDLKHPLLQKYSINDSK 299
 QY 251 RRENPLEMSTYLPITCOLSIGLOSQVPIIANILEVQACW-----GDFQPAETSD 304
 Db 300 SIRGLPREDTYLTP---LSESNSIDATLLQNLVIL---WHGRDPEGIKERLEPGA 350
 QY 305 ILQRRVVAVF---SLSQAVLHHIYIHAHNTAIFQEAHVHKOVSAP--RHQEYLEEG 356
 Db 351 NAEKTLVALYRFKCDYQKELIKQOQVAKKQSISSVSFSKAVSTTPQRRRNESLISV 410
 QY 357 HLCVLEPSVAQHIAHTTASSPLTL-----FSTAI-----PKGLAFRD 394
 Db 411 TSSRRKPISEFKFTASSASSNSLTTPGSSKRLSKNFSSKKLSTIVQSSPTPSRRKRA 470
 QY 395 PALVPRKVPVVDIQAQYNTAKVGLAGYQALRA-----RALDGOELMRGL 443
 Db 471 SVIVNEKQKFAST---FSTTKKRRSSRSIKRMSLIPSKRESVYTKLMSTYAKLAEDD 527
 QY 444 HMVNEVLQATCRRTLEVARSTSLYLSSLSGT-----EFSVSVACTPE---IQELK 490
 Db 528 DW-EYEKEKRT-----SSNFATLIDEIFEYKEYEQIRKEKELEKRVAK 574
 QY 491 AAAL-----RSRLRLAEVLSRCSONITETOESL-----SSLNRELVSQD 533
 Db 575 ARELERRRRRQKEERAKRILE-----KEDLKQKQELKKQJEIDISDEQELSKKEE 629
 QY 534 -----VHERSIOQIOCCD---KMFYIKQFKSKRMAPGIGYNE--EQH 574
 Db 630 KLDGNTSISAPMENNEKNTNHLVEDIDNLLRRNFSLQTRPVSRIDPGIMFSSPTEEVS 689

QY 575 KLDKVNFSH-----LAKRLQVQEECYQKQASLVTHGKMR-----VYHETRNHL 621
 Db 690 PVEKRTENEALTEETKLETLIR---SKFGSSFNIDKEIKLSKMEYPSITAPQRLSEE 746
 QY 622 RLVCQSAACNTAEQVOESLSKLEELSHQLQDRAKGAQASPPPIAP-----Y 671
 Db 747 RVV-----SDSNDGYESL--ILPKDGNVSG--LKSDTATAPVSDRLKISIRV 794
 QY 672 PSPTRKDLLHMOFLCEGMKLLAS-----DLDDNRT---TERLNRPAP 713
 Db 795 PPTFRKS--RHFSESNRLSVLSWYSPKESFTNLVDILKGNLDVNNQDSORIPTP 848

RESULT

7
 C88546
 protein R107.4 [imported] - Caenorhabditis elegans
 C: Species: Caenorhabditis elegans
 C: Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C: Accession: C88546
 R: anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998

A: Title: Genome sequence of the nematode *C. elegans*: a platform for investigating bio
 A: Reference number: A75000; M01D:99069613; PMID:9851916
 A: Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C-
 A: Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
 A: Accession: C88546
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1863 <STO>
 A: Cross-references: GB:chr_III; PIDN:CAA78473.1; PID:93879038; GSPDB:GN00021; CESP:R1
 C: Geneticks:
 A: Gene: R107.4
 A: Map position: 3

Query Match 7.8%; Score 285.5; DB 2; Length 863;
 Best Local Similarity 21.4%; Pred. No. 2.7e-06;
 Matches 168; Conservative 127; Mismatches 269; Indels 221; Gaps 37;

QY 7 YLWHTDDLLGOGATASYKARKKSGELVAVKVFNTSYLRRPREVQVR---EFVLRKL 62
 Db 55 YLTFNDESIKAGVSEYKRT--ESGRVAVK-----ACKKLEVAALIGETELIKL 106
 QY 63 -NHONIVKLFVAEEFGSGROK-----LVMEYSSGSLISVLESPENAFGLPEDEFL-V 114
 Db 107 KGASNIIVQYGSNHTKMAPGSYSETISFAMEYAS--SLEAEKRRKKNRGLSSNALIDL 165
 QY 115 VLVQCVAGMHLRENGIVHRDIKPGNIMLV-----GEGOSITYKLTDFGAARELDD-- 167
 Db 166 VVDCSMA--LSALEHNTAHRDIHNMILLEPGTPTRGRSTHILFKLDCMGCSKSENS 224
 QY 168 EKFSVYGTGEYLHP---DMYRAVL---KPOQKAFGYVDLMSIGVLLYNAAGS 218
 Db 225 HEKRTLVGPNLHPLFAHEMDPLMAQNRNKKTKSATVSEQDLMALGCTLYFCATGK 284
 QY 219 LPTIPFGPRRKEMIR---ITTEKPAAGIAGAOR---RENGPLEMSTYLPIT-- 266
 Db 285 ---FPFEHERNKSLYKHAVALTONPDALVAVLQKGDPRRDIDIEFQ---PVTLEP 338
 QY 267 ---CQSLSIGLSQVPIIANILEVEQAKCWGDFDPAESDILQRRVVVHVSLSQAVLHH 323
 Db 339 AKETRPKMLVSTMCCLLSFHEPSI-----EYAKVADMRSKRTFS----- 384
 QY 324 IYIHAHNTAIFQEA--HKOTSVAVRHQEYLFEGHLCVLEPSVAQHIAHTTASSPLTL 381
 Db 385 -----SVQMSVTEITDSNVP-----HLGFSIPSIS--KCLGPEGGDILL 425
 QY 382 FSTA-----IPKGLAFDPA---LDVPRKPYKVDLQADYNTAKVGLAGYQA 425
 Db 426 SMTSTHYLDKOKSVYDGLPDDLYLVVQPTSHVDMKILAR--NIEFHEPDMDMRKISE 482
 QY 426 LRLAARLLDGOELMRGLHMVNEVLQ--ATCRRTLEVARTSLYLSSLSGT--ERSSVA 481

Db 483 IRIKRC-----YEGSLMTEIDEYALFDPRVSTILSTQSLVQELSOEFERYQTASR 534

Qy 482 -----GPEPE-----IOELKAARELSRLRTLAELVSLSCSQTITET 516

Db 535 FAVYVDMASVPLMLEDEANPEFKMISDOCIQOAKRAREIELERAKVSMIEACAKOLSKD 594

Qy 517 QEGLSLNLEIVKSRQVH-----EDRSIOIOCCIDMNFILYQOFKRSRR 563

Db 595 AEGLRIEDMDLPGICEIESYVFDKQALLSTQKYSQELVEICLKRNNIMEQIFNSP--- 652

Qy 564 PGLGVNEEOIHKLDKYNFSLAK-----RLQVFOECVQKYQASLVTHG 608

Db 653 -----DRINKSLNKAMNLAASLSQLRNSNYRKLDQMISECVDLLE----- 692

Qy 609 KRRRVVHETRN-HLRVCGSVACNTEAGVQ-----ESLSKLEELS 650

Db 693 KPRQEKMDTVNRYLQAGCS---RNTWOKSMHLLRPFHESQIRIKTKYKSCRLLDQLN 749

Qy 651 HOLLO 655

Db 750 TELDQ 754

RESULT 8

S30874

hypothetical protein R107.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Feb-1997

C:Accession: S30874

R:Thomas, K.

submitted to the EMBL Data Library, July 1992

A:Reference number: S30871

A:Accession: S30874

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-795 <THO>

A:Cross-references: EMBL:214092

A:Genetic code:

A:Genetic code: SGCA

A:Initons: 170/1, 237/3, 518/3

C:Keywords: serine/threonine-specific protein kinase

Query Match 7.7%; Score 282.5; DB 2; Length 795;
Best Local Similarity 21.9%; Pred. No. 3.4e-06;
Matches 170; Conservative 121; Mismatches 281; Indels 205; Gaps 37;

Qy 7 YLHHTDILLGGATASYKARKNKSGELVAVKVENTTSYLRPREYQV--REFEVLKRL-N 63

Db 55 YTLFNDSEIGKAYSEVYSGRT-ESGSLVAVK-----TACKKLEVAAGMEIETIKLKG 108

Qy 64 HONIVKLFVAVETGSSRQV-----LVMEYSSGSLVSESPNAGLPEDFEL-VVL 116

Db 109 ASNIVYFGSHHTKMAKPSVTSSETISPMETAYSS-SLEAKSSPKNHSGLSMLLDLYV 167

Qy 117 RCYVAGNHLRENGIVHDIRKGNIMRLV-----GEGQSIVYKLTDFCAARELDDDD--EK 169

Db 168 DCSMA-LGALREHNIADHMKHMINILFPFGPTGRSRTSHFLKIDMCSKSLSSNSHS 226

Qy 170 FVSIVGTGEYVLR-----DMYERAVLR-----KPOOKAGVAVDLSISVTLTYHAATGSLP 220

Db 227 MSTLVGTNLLHPLAHNEKVPDLMAQNSHNMKTSAYTSECCDMLALCTILFPCATGR-- 284

Qy 221 FLPEGGPRRKEIYR-----ITTEKPAAGIAGQR-RENGPLEVSYTLPTCOISLIGLOS 275

Db 285 -PFPFHESNNKSLYHKAVALLQNDALAMVLVQKGRDPSGTDMEFQPYTEL----- 337

Qy 276 OLVPILANILEYQAKCGFDQFAETSDIQRVYVYVYFSLSQVLAHHIYIHAHTIALF 335

Db 338 -----PAKFTSYPRMIVSTMTCLRSFPHESI-----EYAKAVADAMSNS 378

Qy 336 QEAIVHK-----QTSVAPRHOEYILEGHLCVLEPVSQNHIAHTTASSPLTLESTA----- 385

Db 379 KRSTFSSVDQMSIV-EHTDMSNVPHLGFSPISIS-KCLGPEGTDMLLSNTSTHYLDSK 436

Qy 386 -----IPKGLAFRPA---LDVPKEVPKVDLQADYNTAKGVLAGVQALRLARALLDQ 436

Db 437 QKSVGLPDLQVLPVQPSHYVMSKILAS---NIEFHEPDMTDSKLEIRKRC----- 488

Qy 437 ELMFGLHVMVEVLQ--ATCRRTELVARTSLYLSSSLGT-ERFSSVA----- 481

Db 489 ---YGLSLMTEIDEYALFDPRVSTILSTQSLVQELSOEFERYQTASRAVYVDMASVP 545

Qy 482 -----GPEPE-----IOELKAARELSRLRTLAELVSLSCSQTITET 524

Db 546 LMLFDEANPEFKMISDOCIQOAKRASE---ELSHAKVSMIEACAKOLSKAEPLRED 602

Qy 525 RELVYSRDQVH-----EDRSIOIOCCIDMNFILYQOFKRSRRRGVLYNE 571

Db 603 MDLPGICEIESYVFDKQALLSTQKYSQELVEICLKRNNIMEQIFNSP----- 652

Qy 572 QIHKLDKYNFSLAK-----RLQVFOECVQKYQASLVTHGKRRRVYHE 616

Db 653 -----DSMNKSKLNKAMNLAASLSQLRNSNYRKLDQMISECVDLLE-----KPRQEKMD 700

Qy 617 TRN-HLRVCGSVACNTEAGVQ-----ESLSKLEELS 655

Db 701 TVNRYLQAGCS---RNTWOKSMHLLRPFHESQIRIKTKYKSCRLLDQ 754

RESULT 9

S56639

ribosomal protein S6 kinase homolog (clone Aspkl1) - oat

N:Alternate names: mitogen-activated protein kinase pf70 homolog

C:Species: Avena sativa (oat)

C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999

C:Accession: S56639

R:Huttlly, A.K.; Phillips, A.L.

Plant Mol. Biol. 27, 1043-1052, 1995

A>Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that s

A:Reference number: S56638; MUID:95284341

A:Accession: S56639

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-480 <HUT>

A:Cross-references: EMBL:X79992; NID:g871985; PION:CA5613.1; PID:g871986

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C:Keywords: ATP; phosphotransferase; protein kinase

F:149-407/Domain: protein kinase homology <KIN>

F:157-165/Region: protein kinase ATP-binding motif

Query Match 7.6%; Score 281; DB 2; Length 480;
Best Local Similarity 26.3%; Pred. No. 2.3e-06;
Matches 102; Conservative 61; Mismatches 147; Indels 78; Gaps 15;

Qy 14 LLGGATASYKARKNKSGELVAVKVENTTSYLRPR--EYQVFEFEVLRKLNQNTVKLF 71

Db 156 LVGGAGFGKYQVYMKTSSEIYAKVKRDKILEKNIAEYMKAREDLITFVDHPFVYQLR 215

Qy 72 AVEETGSSRQVLYMEYSSGSLVSESPNAGLPEDFELVYLR--VYAGNHLRENG 130

Db 216 YSFQT--KYRLYLVLDDVNGHLEFQLYQO---GLFREELARLYTAIEIVSVAHLHANG 269

Qy 131 IVHNDIRPGNIMRLVGEQSGIYKLTDFGAARELDDDEKFSVYGTGEYVLRPDYERAVL 190

Db 270 IMHBDLRENT--LDDARGHAM--LTPGLAKEDEMTSRSMGCTVEYAPAEIV----- 320

Qy 191 RKPOOKAFGVYVDLSIGVTLTYHAATGSLPFIPEGPRRKEIYRITTEKPAAGIAGAQ 250

Db 321 ---QGRGHDKAQDMWVGILLFEMLTGKPP--FGNR--DKIQOKIVREK----- 364

Qy 251 RRENGPLEWSTTLPTTQOLSLGLOSQVPLIANLLEVEQAKCGMDFQFAETSDIQRV 310

Db 365 -----MKLPYSLSSEVHSILKGLHREAGKRLGSG----- 394

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QY 311 VHVFSLSQAVLHHIYTHAHTAIFQEAHVAKQTSVAPRHOEYLFEGHLCV--LEPSVSAQ 368
Db 395 ---LGSDSDIKKHKMKFAVMKRL--EAKIQSPFCPN-----VAGQCIANFDCWISM 444
QY 369 HIAHTASSPLTFLSPALPKGLAFDPA 396
Db 445 PYLDSPVSPVAADSNEF--GFSYVRPA 470

RESULT 10
S61137
Probable membrane protein YGL180W - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G1615
C:Species: Saccharomyces cerevisiae
C:Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1999
C:Accession: S61137; S64197
R:Bertani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Bruschi, C.V.
submitted to the EMBL Data Library, September 1995
A:Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm of S.cet
live new genes.
A:Reference number: S61128
A:Accession: S61137
A:Molecule type: DNA
A:Residues: 1-897 <BER>
A:Cross-references: EMBL:X91489; NID:q1143557; PIDN:CAA62794.1; PID:q19059; PID:q114356
R:Brusch, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64183
A:Accession: S64197
A:Molecule type: DNA
A:Residues: 1-897 <BRU>
A:Cross-references: EMBL:Z72702; NID:q1322790; PIDN:CAA96892.1; PID:e243788; PID:q132279
C:Genetics:
A:Gene: SGD:APC1
A:Cross-references: SGD:S0003148; MIPS:YGL180W
A:Map position: 7L
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; transmembrane protein
F:22-325/Domain: protein kinase homology <KIN>
F:30-38/Region: protein kinase ATP-binding motif
F:65-71/Domain: transmembrane #status predicted <TM>

Query Match 7.6%; Score 281; DB 2; Length 897;
Best Local Similarity 20.2%; Pred. No. 4.5e-06;
Matches 177; Conservative 124; Mismatches 315; Indels 262; Gaps 34;

QY 1 MGSANTLMTDDLLGGGATASYKAR-NKSGELVAVKVFNTSYLRPREVQREPE-- 57
Db 18 MASGANT--AEKEIGKGFAYVRCGLTSDKSOHVAIKVSHAKLKNKLENLLEIETA 75
QY 58 VLKRLNQNIVKLEAVEERGSGQKVLVMEYCGSSGLSTLSE----- 99
Db 76 ILKKIKRPHVGLDCERT--STDFTYLMYCALGDLTFLKRRKELMENNPLRTVFEK 133
QY 100 ---SPENAFGLPDEFLVYLRCVAGMNLRENGIVHRIKPKPNI----- 141
Db 134 YPPSEHNHNLHRAFLVSYLOQLASALKFLRSKNLVHRIKPKPNIPLIGYHDSKSF 193
QY 142 --WRLVGEESQSIYKLTLDGAARELDDDEKFEVSYGTEELHEDM--YERAVLRKPKQKA 197
Db 194 HELGFVGIYNLPILKTIADFGFARFLPNTSLAETLCSGLPYMAPELLNYOK----- 243
QY 198 FGVTYVLMISGVTLYMAAGSGLPFIFFGGRPRRKELMTYTEKPRGALTAGAQRRENGPL 257
Db 244 YNKAADLMSVGYVEMCGTPEF---RASNHELEFKI-----KRANDVI 286
QY 258 EMSYTLPTICOLSLQOSLDVPLANILVEQAKGKGFOPFA-----ETSDTL 306
Db 287 ---TFPVC---NIEPELKEICSLFLPDAQRIGEFEFFANRVNEDLSSYELEDL 338
QY 307 -----QRYVHVFSLSQAVLHHIYTHAHT 331

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Db 339 PELESKSGIVESNMFVSEYLSKQKSPNSNLTGHQSMADNPALSDALKNSNLTAPAV 398
QY 332 IAIQEAHVAKQTSVAPRHOEYL-----FEGLHCYLE-PSYSAQHA-----H 372
Db 399 KTDHTQAVDKKASNNKHNLSVDSRSEFREVYVEKKSIVNSLADAEVAGNPPIKH 458
QY 373 TTAS-----SPLTLESTAIPRG-----LAFRDPAIDVRK 401
Db 459 PTTQONQNVLLNEQSPNNQOYFQNGENPRLRATSSSGSGDGNRPSLVDRRLSIS 518
QY 402 FVPYVDLQADYVPAKVL--GAGYQALR-----LARLLDQGLMERGL--HWMEY 449
Db 519 LNPENALSRNLGLASTLFEFGAQQQQQQQITSSPPYSQLLNSQ--LHELENTLIRI 576
QY 450 LQATCRRTLEVARTSLYLSSSLGTE-----RFSVAGTPEIOELKAAEIRSLR 499
Db 577 DHLQHPETTLKIDMNTVSILESIAAKAFVYSYAEVKFSQI--VPLSTTLKGANENR- 633
QY 500 RLAEVLSRCSQNTTEQESLSLNEELVKSROVHEDNSIQOI-QCCIDKNMFIYKQPK 558
Db 634 -----RSMDSNAIAEED-----SDAEEDDEFLKKYKEDCLSTKTF----- 670
QY 559 KSRMRPGLGYNEQIHKLDKVFNSHLAKRLLYQFQECYQKQASLVTHGKMRVYHETR 618
Db 671 -----GKGRTLATSQGL-SATFNKLPRESEMILLCEALVLYMKALSTLSKQVTSNMW 723
QY 619 NHRIVGCSVAACNTEAGVQESLSKLEB-----LSHQLLDQRAK 659
Db 724 YESQEKSCSLRV-NVLQWLRKEFNECLEKADFLRKINDLRFKHSVEAENQITL--K 780
QY 660 GAQASPPPIAPYSPTRKDLLHMOELCEGMKLASDL 697
Db 781 GSSEEP-----VYLEKLLYDRALEISKMAAHMELKGENL 814

RESULT 11
A39616
Protein kinase RAD53 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein P2588; protein YPL153c; Spk1 protein
C:Species: Saccharomyces cerevisiae
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jul-2000
C:Accession: A39616; S65164; S69446; S13321
R:Zheng, D.F.; Zheng, P.; Beldier, D.R.; Zerillo, C.
Mol. Cell. Biol. 13, 5829-5842, 1993
A:Title: Spk1 is an essential S-phase-specific gene of Saccharomyces cerevisiae that
submitted to the Protein Sequence Database, May 1996
A:Reference number: A39616; MUID:91117267
A:Accession: A39616
A:Molecule type: DNA
A:Residues: 1-821 <STE>
A:Cross-references: GB:M55623; NID:q172656; PIDN:AAA5070.1; PID:q172657
A:Experimental source: strain S288C
R:Zheng, P.; Fay, D.S.; Burton, J.; Xiao, H.; Pinkham, J.L.; Stern, D.F.
Mol. Cell. Biol. 13, 5829-5842, 1993
A:Title: Spk1 is an essential S-phase-specific gene of Saccharomyces cerevisiae that
submitted to the Protein Sequence Database, May 1996
A:Reference number: A39616; MUID:91117267
A:Accession: A39616
A:Molecule type: DNA
A:Residues: 1-821 <PUN>
A:Cross-references: EMBL:Z73509; NID:q1370325; PIDN:CAA97858.1; PID:q1370326; GSPDB:G
A:Experimental source: strain S288C (AB972)
R:Punelle, B.; Comblez, S.; Coster, F.; Naveau, F.; Goffeau, A.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifi
ogue to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the pI
A:Reference number: S69446
A:Accession: S69446
A:Molecule type: DNA
A:Residues: 1-821 <PUN>

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Query Match 7.58; Score 274; DB 2; Length 1231;
 Best Local Similarity 21.6%; Pred. No. 1.4e-05;
 Matches 169; Conservative 107; Mismatches 280; Indels 228; Gaps 37;

QY 9 WHTDILGCGATATSVYKARKKSGELVAVKNTSTYLRPREVOYREFEVRLKLNHONIV 68
 DB 34 WETIGELDGGAFGKYKKQNKETINVLAAKYIDTKSEELDYAV-ETDILASCDHPNIV 92
 QY 69 KL-FAVEETGSRQKVLVMEYCSGSLVS-LESPEAFGLPEDEFLVLRVAVAG 122
 DB 93 KLIAFAFYE-----NNMLILIEFCAGAVDAVMLELERP-----LTSQIQVYCKQLLEA 142
 QY 123 MNHLRENGIVHRDIKPGNIM-RLVGEESQSYKLTDEGA-RELDDEKFSVYGT 177
 DB 143 LNYLHDMNTHIRDLKAGNILEFTLDG-----IKLADFGVSAKRNRTIQRDSFT- 194
 QY 178 EYLHPDMYERAVLRKPOQKAGVIVYDLSIGVTLVHAATGSLPPIPGPRRNKEIMYRI 237
 DB 195 YMAAPEV---VMCEFSKDRPYDYKADVMSLGITILEMAETPPHNL-NPWR--VLTKI 247
 QY 238 TTEKPAAGIAGAQRENGPLEWSTLPTICQLSIGLSQVLPIANILEVQAKMGFDQ 297
 DB 248 AKSEPPYL-AQ-----PSRMS-----SNEKDFLKCLEKNVDARW- 281
 QY 298 FFATSDILQRYVYVFSLSQAVLHNYIHA-----NHTIAL-FQ 336
 DB 282 ---TTSQLOHPRVYTIID-SKKPIRELIARAKAEVTEVEDGKEEDDEETENSLPITN 336
 QY 337 EAVHKQTSVAPRHOEYLFEGHLCVLEPSVAQNIHAHTTASSPLTLFSTAI-----P 387
 DB 337 KRASSDLSIASSEEDKLSQ-NACILE-SVS-EKTEHNASGD-KFSTKVLNKPCEGP 390
 QY 388 KG-----LAFRDALDVPK-----VPKYDLADYTAAGVLAGAGYQALRLARALL 433
 DB 391 ENAVELVGAVAVLPDRAVELPESGREKRPKIDRLPDTED-----QEMADINSVS 441
 QY 434 DGOELMRGLHWMEVYLOATCRTELEARTSLTYLSSLTERRFSSVAGTPELOELKAA 493
 DB 442 EGEE-----DHAVYSEINIEHNLKPEKERQEKOPVLEKWLVS 480
 QY 494 ELRSRLTIAEVLRSQNTTEQESLSLNRLELVSRQVHEDRSIQOCCLDKMNFI 553
 DB 481 E-----DTTQYDVLVSQETGEKEVDHILDSVNAVEDTHEK-----LRDDDT 526
 QY 554 YKQFKSRMRPGLYNEEOIHKLDKYNFSL-----AKRLQVQOEBCVQKQAS 603
 DB 527 QKVYISD-TSSVGERDEELGAVPKTAESSAEGAQDGKETEDEGAQILISKATEGPAS 584
 QY 604 -----LV--THGKRMRVYHETR-NHLRLVGSVAACNTEAGVQE 640
 DB 585 GTEEAPRYTEITETNDTDOKLVENHCKOLPISSETTLTDSGLASSEGREVTESSGTE 644
 QY 641 -SLSKLLELSHOLLDRAKGA-----QASPPPIA 669
 DB 645 VEVEGAVSETDEEDVQSETRGAPMAVYOMTEKNETPHEAPAVEVQVPPQSEPPIA 704
 QY 670 PYPS 673
 DB 705 PIPS 708

RESULT 14
 A48084
 STE11 protein kinase homolog NP1 - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 19-Dec-1997
 C:Accession: A48084
 R:Banno, H.; Hirano, K.; Nakamura, T.; Irie, K.; Nomoto, S.; Matsumoto, K.; Machida, Y.
 Mol. Cell. Biol. 13, 4745-4752, 1993
 A:Title: NP1, a tobacco gene that encodes a protein with a domain homologous to yeast P
 A:Reference number: A48084; MUID:93330268
 A:Status: preliminary

A:Molecule type: nucleic acid
 A:Residues: 1-706 <BAN>
 A:Experimental source: By-2 cells
 A:Note: sequence extracted from NCBI backbone (NCBIN:135697, NCBI:135698)
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
 C:Keywords: ATP
 F:94-358/Domain: protein kinase homology <KIN>
 F:102-110/Region: protein kinase ATP-binding motif

Query Match 7.4%; Score 273.5; DB 2; Length 706;
 Best Local Similarity 21.0%; Pred. No. 7.8e-06;
 Matches 165; Conservative 109; Mismatches 235; Indels 277; Gaps 40;

QY 9 WHTDILGCGATATSVYKARKKSGELVAVK-VENTSTYLRPREVOYREFE-VLR 60
 DB 96 WRKGEIMIGCAFEGRYVMGNMVDGELLATKEVSIANGASRRER-AQAHVRELEEVNLLK 154
 QY 61 KLNHONIVKLFAVEETGSRQKVLVMEYCSGSLVSLESPEAFGLPEDEFLVLRVAVAG 119
 DB 155 NLSHPNIVRVLGTRARAGSLN-ILIEFVPGGSISL--GKFGSPESVYIRMTYKOL 208
 QY 120 VAGMHLRENGIVHRDIKPGNIMRLVGEESQSYKLTDEGAAR-ELDDDEKFSVYGT 176
 DB 209 LIGLEYLHKNIGIMHRDIKGANI-LVDNKG-CIKLADGASKVVELATMTGAKSMKG 264
 QY 177 EYLHPDMYERAVLRKPOQKAGVIVYDLSIGVTLVHAATGSLPPIPGPRRNKEI-M 234
 DB 265 PYMAPEV-----LDTGHSFSDIWSVCGTITTEMAETGPPW-----SQOYQEVAA 311
 QY 235 YRTTEKPAAGIAGAQRENGPLEWSTLPTICQLSIGLSQVLPIANILEVQAKMG 294
 DB 312 FHIGTK-----SHD-----PIPEHNS----- 328
 QY 295 PQGFETSDILQRYV-VHVFSLQAVLHNYIHAHTTASSPLTLFSTAI-PKGLAPDPAVDY-PKVPKVDQA 351
 DB 329 ---AESKDFLKCLEKPEHILRHASNLIQHPFYTA-----EHQ 364
 QY 352 YLFEGHLCVLEPSVAQNIHAHTTASSPLTLFSTAI-PKGLAPDPAVDY-PKVPKVDQA 410
 DB 365 -----ARFLSSSPGN-----PENMAAO-RMDVRTSIIP-DMRA 397
 QY 411 DYNIAKGVLAGAYQALRLARALLDGOELMRGLHWMEVYLOATCRTELEARTSLTYLSS 470
 DB 398 SCNGLKDVCG-----VSAVRCSTVYPEN 420
 QY 471 SLGTERFSSVAGTPELO-----ELKAAAEILRS-RLKTLAR- 504
 DB 421 SLGKESLMKLGNSDDDMCOMNDDEFMGASVYCSDDLSPANKYSFPMCEPDNDWPKCF 480
 QY 505 ---VLSRCSQNTTEQESLSLNRLELVSRQV-HEDESIQOIQCL 547
 DB 481 DESPELTGKSOANLHYDQATIKPTNPIWSYKEDLAFPPSGQSAAEDEDELTESKIAFL 540
 QY 548 DKMNITYQFK-----KSRMRP-GLGYNEQIHKLDKYNF-----SLA 585
 DB 541 DEKANDLKKIQTPLYEGYNSLWSTPSPVGTG-NKENVP--SNINLPKRSRPKRLMS 597
 QY 586 KRLQVFOECVQKQOASIVTHGKRM-----RVVHEPR-----NHLR-LVYGSVACN 632
 DB 598 RRLSTALIGACA---PSPVTHSKRISITIGLNEALIOEAOIPLRHNHMKDILGQREAVN 653
 QY 633 TEAGVOESLSKLELSHOLLDRAKGAQ--SPPPIAPYSPTRKDLNLHNOELCEG 689
 DB 654 S---SFSERQRWRKEIIDEIQRKREIMRQVNLSP-----KDIILNR--CRS 697
 QY 690 MKLLAS 695
 DB 698 KSRPAS 703

RESULT 15
 B96716

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 14, 2002, 13:16:47 ; Search time 66.66 Seconds
(without alignments)
415.890 Million cell updates/sec

Title: US-09-582-397A-2

File: 3674
Sequence: 1 MOSTANYLMTDLDLGGAR.....LDNNRIERLNKVPAPDV 716

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	3674	100.0	716 1 IKKE_HUMAN	014164 homo sapien
2	3102.5	84.4	717 1 IKKE_MOUSE	097018 mus musculu
3	424.5	11.6	757 1 IKRB_MOUSE	088351 mus musculu
4	424	11.5	756 1 IKRB_HUMAN	014920 homo sapien
5	414.5	11.3	757 1 IKRB_RAT	094778 rattus norv
6	399.5	10.9	745 1 IKRA_MOUSE	060680 m inhibitor
7	391	10.6	745 1 IKRA_HUMAN	015111 h inhibitor
8	305.5	8.3	1051 1 ULK1_MOUSE	070405 mus musculu
9	303.5	8.3	1050 1 ULK1_HUMAN	075385 homo sapien
10	299	8.1	1050 1 Y537_HUMAN	060285 homo sapien
11	286.5	7.8	713 1 KP78_HUMAN	P27448 homo sapien
12	286.5	7.8	1142 1 GINA_YEAST	012263 saccharomyc
13	286	7.8	966 1 ST10_MOUSE	055098 mus musculu
14	285.5	7.8	863 1 YNHA_CAEEL	P32742 caenorhabdi
15	281	7.6	897 1 APE1_YEAST	P53104 saccharomyc
16	280	7.6	776 1 SNIL_RAT	097105 rattus norv
17	278.5	7.6	779 1 SNIL_MOUSE	060670 mus musculu
18	276	7.5	821 1 SPK1_YEAST	P22116 saccharomyc
19	275	7.5	915 1 KC4_YEAST	P25389 saccharomyc
20	275	7.5	968 1 ST10_HUMAN	094804 homo sapien
21	267.5	7.3	880 1 KPCN_HUMAN	094806 homo sapien
22	267.5	7.3	1431 1 DAPK_HUMAN	P53353 homo sapien
23	267	7.3	487 1 STR4_HUMAN	013043 homo sapien
24	266.5	7.3	918 1 KPCN_MOUSE	062101 mus musculu
25	266.5	7.3	1436 1 WNI_SCHPO	074304 schizosacch
26	266	7.2	445 1 MEK1_SCHPO	010592 schizosacch
27	266	7.2	733 1 K6A1_SCHPO	015492 homo sapien
28	265.5	7.2	465 1 KPA1_ARATH	P42818 arabidopsis
29	265	7.2	735 1 K6A1_HUMAN	015418 homo sapien
30	264	7.2	1062 1 CC7_SCHPO	P41892 schizosacch
31	263.5	7.2	471 1 KPI9_ARATH	Q39030 arabidopsis
32	263.5	7.2	774 1 KEMK_MOUSE	005512 mus musculu
33	263.5	7.2	912 1 KPCN_HUMAN	015139 homo sapien

34	263	7.2	733 1 K6A1_XENLA	P10665 xenopus lae
35	262.5	7.1	658 1 PAK1_SCHPO	P50527 schizosacch
36	262.5	7.1	714 1 HUNK_HUMAN	P57058 homo sapien
37	262	7.1	856 1 UN51_CAEEL	Q23023 caenorhabdi
38	262	7.1	1142 1 PAK1_YEAST	P38990 saccharomyc
39	261	7.1	629 1 K6AB_XENLA	P10666 xenopus lae
40	260.5	7.1	714 1 HUNK_MOUSE	088866 mus musculu
41	260	7.1	735 1 K6A1_RAT	063531 rattus norv
42	260	7.1	1030 1 STR9_HUMAN	076039 homo sapien
43	260	7.1	1314 1 S522_YEAST	P25390 saccharomyc
44	258	7.0	386 1 KPBG_HUMAN	Q16816 homo sapien
45	258	7.0	491 1 STR3_HUMAN	Q13188 homo sapien

ALIGNMENTS

RESULT 1
ID IKKE_HUMAN STANDARD; PRT; 716 AA.
AC 014164;
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 16-OCT-2001 (Rel. 41, last annotation update)
DT 01-MAR-2002 (Rel. 41, last annotation update)
DE Inhibitor of nuclear factor kappa-B kinase epsilon subunit
DE (EC 2.7.1.-) (I kappa-B kinase epsilon) (IKBE) (IKK-epsilon) (IKK-E)
DE (inducible I kappa-B kinase) (IKK-1).
GN IKBE OR IKKE OR IKKI OR KIA00151.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-38; GLU-168 AND SER-172.
RX MEDLINE=99352266; PubMed=10421793;
RA Shimada T., Kawai T., Takeda K., Matsumoto M., Inoue J.-I.,
RT "IKK-1, a novel lipopolysaccharide-inducible kinase that is related to
RT IkappaB kinases.";
RL Int. Immunol. 11:1357-1362(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=20337984; PubMed=10882136;
RA Peters R.T., Liao S.-M., Mantatis T.,
RT "IKK epsilon is part of a novel PMA-inducible IkappaB kinase
RT complex.";
RL Mol. Cell 5:513-522(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96127530; PubMed=8590280;
RA Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.,
RT "Prediction of the coding sequences of unidentified human genes. IV.
RT The coding sequences of 40 new genes (KIA0121-KIA0160) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 2:167-174(1995).
RN [4]
RP FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
RN ULTIMATELY THE DEGRADATION OF THE INHIBITOR. MAY PLAY A SPECIAL
RN ROLE IN THE IMMUNE RESPONSE.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SPLEEN FOLLOWED BY THYMUS,
CC PERIPHERAL BLOOD LEUKOCYTES, PANCREAS, PLACENTA. WEAKLY EXPRESSED
CC IN LUNG, KIDNEY, PROSTATE, OVARY AND COLON.
CC -I- PFM: AUTOPHOSPHORYLATED.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC IKAPAB KINASE SUBFAMILY.
CC
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CC EMBL: D63485: BAA09772.1: -
 CC EMBL: AB016590: BAA85155.1: -
 CC EMBL: AF241789: AAF45307.1: -
 DR MIM: 605048: -
 DR InterPro: IPR000719: Euk_pkinase.
 DR InterPro: IPR002290: Ser_thr_pkinase.
 DR Pfam: PF00069: pkinase.1.
 DR PROSITE: PS00107: PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00108: PROTEIN_KINASE_ST.FALSE.NEG.
 DR PROSITE: PS0011: PROTEIN_KINASE_DOM.1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 9 315 PROTEIN KINASE.
 FT DOMAIN 436 457 LEUCINE-ZIPPER (POTENTIAL).
 FT NP_BIND 15 23 ATP (BY SIMILARITY).
 FT BINDING 38 38 ATP (BY SIMILARITY).
 FT ACT_SITE 135 135 BY SIMILARITY.
 FT MOD_RES 172 172 PHOSPHORYLATION.
 FT MUTAGEN 38 38 K->A: LOSS OF KINASE ACTIVITY.
 FT MUTAGEN 168 168 E->A: SLIGHT DECREASE OF KINASE ACTIVITY.
 FT MUTAGEN 172 172 S->A: LOSS OF AUTOPHOSPHORYLATION AND OF KINASE ACTIVITY.
 FT MUTAGEN 172 172 S->E: DECREASE IN KINASE ACTIVITY.
 SQ SEQUENCE 716 AA; 80462 MW; 3E5FE5840734D81 CRC64;

Query Match 100.0%; Score 3674; DB 1; Length 716;
 Best Local Similarity 100.0%; Pred. No.9.5e-220;
 Matches 716; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOSTANTLMHTDLDLGGATASYKANKKSGELVAVKVENTSYLPRREYOVEEFLVR 60
 DB 1 MOSTANTLMHTDLDLGGATASYKANKKSGELVAVKVENTSYLPRREYOVEEFLVR 60
 QY 61 KLNQNTVYKLFVAVENGSGKQKLYVMYCGSSGLSTVLESPENAFGLPEDEFLVLCVV 120
 DB 61 KLNQNTVYKLFVAVENGSGKQKLYVMYCGSSGLSTVLESPENAFGLPEDEFLVLCVV 120
 QY 121 AGNNHLRENGIVHRDIKPGNIMRLVGEESQSYKLPFGARELDDDEKVVSYGTEYL 180
 DB 121 AGNNHLRENGIVHRDIKPGNIMRLVGEESQSYKLPFGARELDDDEKVVSYGTEYL 180
 QY 181 HPDMYEAVALRKPOQKAFGYTVDLMSIGVTLVYAAFGSLPFIFFGGPRRNKEIMYRITTE 240
 DB 181 HPDMYEAVALRKPOQKAFGYTVDLMSIGVTLVYAAFGSLPFIFFGGPRRNKEIMYRITTE 240
 QY 241 KPAGAIAGAORRENGPLEMSYTLPTICQLSLGLOSQVPLANILVEQAKCGEFOFRA 300
 DB 241 KPAGAIAGAORRENGPLEMSYTLPTICQLSLGLOSQVPLANILVEQAKCGEFOFRA 300
 QY 301 ETSDDILQVVVHVFSLSQAVLHHITVIAHNTLAIPOEAVHKQTSVAPRHOEYLFEGHLCV 360
 DB 301 ETSDDILQVVVHVFSLSQAVLHHITVIAHNTLAIPOEAVHKQTSVAPRHOEYLFEGHLCV 360
 QY 361 LEPSSVAOHIAHTTASSPLTFSTALPKGLAFRDPALDVPKPYKVDLQADYNTAKVGLG 420
 DB 361 LEPSSVAOHIAHTTASSPLTFSTALPKGLAFRDPALDVPKPYKVDLQADYNTAKVGLG 420
 QY 421 AGYQALRLRALDGOELFMFGHVMVEYLQATCRTELEVARTSLYSSSLGTERESSV 480
 DB 421 AGYQALRLRALDGOELFMFGHVMVEYLQATCRTELEVARTSLYSSSLGTERESSV 480
 QY 481 AGPELQELKAAAELESLRLTAELVSRCSQNTTETQESLSLNLRELVSROQVHEDRSI 540
 DB 481 AGPELQELKAAAELESLRLTAELVSRCSQNTTETQESLSLNLRELVSROQVHEDRSI 540
 QY 541 OOIQCCCLDMKNFTYKQFKSRMRPGIGYNEOIHKLDKVNFSLHAKRLQLQVQEECVQKY 600
 DB 541 OOIQCCCLDMKNFTYKQFKSRMRPGIGYNEOIHKLDKVNFSLHAKRLQLQVQEECVQKY 600

QY 601 QASLVTHGKRRVYHETRNHLRLVGCVAACNTAAGVQESLSKLELSHQLDRAGK 660
 DB 601 QASLVTHGKRRVYHETRNHLRLVGCVAACNTAAGVQESLSKLELSHQLDRAGK 660
 QY 661 AQAAPPPIAPYSPTRKDLLHMOELCEGKMLASLDLNNRITELRNVPAPDV 716
 DB 661 AQAAPPPIAPYSPTRKDLLHMOELCEGKMLASLDLNNRITELRNVPAPDV 716

RESULT 2
 ID IKKE_MOUSE STANDARD; PRT; 717 AA.
 AC 09OCT8;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase epsilon subunit
 DE (EC 2.7.1.-) (I kappa-B kinase epsilon) (IKKE) (IKK-epsilon) (IKK-E)
 DE (Inducible I kappa-B kinase) (IKK-I).
 GN IKKE OR IKKE OR IKKI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Macrophage;
 RA MEDLINE=93532266; PubMed=10421793;
 RA Shinoda T., Kawai T., Nakeda K., Matsumoto M., Inoue J.-I.,
 RA Tatsumi Y., Kanamaru A., Akira S.;
 RT IKK-I, a novel lipopolysaccharide-inducible kinase that is related to
 RT IkappaB kinases.";
 RL Int. Immunol. 11:1357-1362(1999).
 CC -I- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR. MAY PLAY A SPECIAL
 CC ROLE IN THE IMMUNE RESPONSE (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (probable).
 CC -I- INDUCTION: BY LIPOLYSACCHARIDE (LPS).
 CC -I- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPA-B KINASE SUBFAMILY.
 CC
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CC EMBL: AB016589: BAA85154.1: -
 DR MGI: 1929612: Ikke.
 DR InterPro: IPR000719: Euk_pkinase.
 DR InterPro: IPR002290: Ser_thr_pkinase.
 DR Pfam: PF00069: pkinase.1.
 DR PROSITE: PS00107: PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00108: PROTEIN_KINASE_ST.FALSE.NEG.
 DR PROSITE: PS0011: PROTEIN_KINASE_DOM.1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 9 315 PROTEIN KINASE.
 FT DOMAIN 452 473 LEUCINE-ZIPPER (POTENTIAL).
 FT NP_BIND 15 23 ATP (BY SIMILARITY).
 FT BINDING 38 38 ATP (BY SIMILARITY).
 FT ACT_SITE 135 135 BY SIMILARITY.
 FT MOD_RES 172 172 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 717 AA; 80939 MW; 3863E0A0FAB997D3 CRC64;

Query Match 84.4%; Score 3102.5; DB 1; Length 717;
 Best Local Similarity 82.7%; Pred. No.1.9e-184;

Matches 596; Conservative 58; Mismatches 58; Indels 9; Gaps 4;

QY 1 MOSTATYLVHTDLDLGCGATASVYKRNKSGELVAVKVFNTSYLRPEVOYREEVLR 60
 DB 1 MOSTATYLVHTDLDLGCGATASVYKRNKSGELVAVKVFNTSYLRPEVOYREEVLR 60
 QY 61 KLNHONIVLFAVEETGSSROKVLVMEYCSGSLSVLESPENAFGLPDEFLVLCVY 120
 DB 61 KLNHONIVLFAVEETGSSROKVLVMEYCSGSLSVLESPENAFGLPDEFLVLCVY 120
 QY 121 AGNHLRENGCIYHRDIPGKINMLVGEEOQSYIKLDFGAAKRLDDEKVFYVYGTDEYL 180
 DB 121 AGNHLRENGCIYHRDIPGKINMLVGEEOQSYIKLDFGAAKRLDDEKVFYVYGTDEYL 180
 QY 181 HPMTYERAVLRKPOKAFGVTVLMSIGVLYLHAATGSLPFIPEGSPRRNKETMYRTTE 240
 DB 181 HPMTYERAVLRKPOKAFGVTVLMSIGVLYLHAATGSLPFIPEGSPRRNKETMYRTTE 240
 QY 241 KPAAGATAGORRENGPLVMSYTLPTICQLSLGSLQSLVPLIANILEVEQAKCWGFQDFA 300
 DB 241 KPAAGATAGORRENGPLVMSYTLPTICQLSLGSLQSLVPLIANILEVEQAKCWGFQDFA 300
 QY 301 ETSIDILQRRVAVVFSLSQAVLHHIYTHAHNTAIPOEAVHAKOTSVAPRHOEYLFEGHLCY 360
 DB 301 ETSIDILQRRVAVVFSLSQAVLHHIYTHAHNTAIPOEAVHAKOTSVAPRHOEYLFEGHLCY 360
 QY 361 LEPSSVNOHIAHTTASSPLTLFSTA--IPKGLAFRDPALDPKFKVDLQADYNTAKGV 418
 DB 361 LEPSSVNOHIAHTTASSPLTLFSTA--IPKGLAFRDPALDPKFKVDLQADYNTAKGV 420
 QY 419 LGAGYQALRLARLLDGOELMFRGLHVMVEYLQATCRLEVARLSILYSSSLGTERFS 478
 DB 421 LGAGYQALRLARLLDGOELMFRGLHVMVEYLQATCRLEVARLSILYSSSLGTERFS 480
 QY 479 SVAGTPEIOELKAAELRSRLRLAEVLSRCSNITPTOESLSLNEKSRDOYVED 537
 DB 481 SVAGTPEIOELKAAELRSRLRLAEVLSRCSNITPTOESLSLNEKSRDOYVED 540
 QY 538 RSTIOQLCCLDKMFYIKPKRKSRRPGLGYNBQIHKLDKVFNSHLAKRLLOVFOECY 597
 DB 541 KSIQICCCLDKMFYIKPKRKSRRPGLGYNBQIHKLDKVFNSHLAKRLLOVFOECY 600
 QY 598 QKYVASLVTHGKRVRVYHETRNHLRVGCSVACNTAOGVQESLKLDELSHQLQDR 657
 DB 601 QKYVASLVTHGKRVRVYHETRNHLRVGCSVACNTAOGVQESLKLDELSHQLQDR 656
 QY 658 A--GAOASPPPIAPDPSPRKLRLHMOELCEGMLKLASLDLDNNRIERLNVAPAPD 715
 DB 657 ASEGGAEVSHQPMAPHPGPDPKDLVFMQELCNDMKLLADLDQNNRIERLNVAPAPD 716
 QY 716 V 716
 DB 717 V 717

RESULT 3
 ID IKRB_MOUSE STANDARD; PRT; 757 AA.
 AC 088351: 09R1J6; (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-B) (1-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEK1.
 RC STRAIN=C57BL/6; TISSUE=Spleen;

RX MEDLINE=98186238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RA Okumura K.;
 RT "Differential regulation of I-kappaB kinase alpha and beta by two
 RT upstream kinases: NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase-1";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RT "Murine I-kB kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of I-kB";
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinases-1 (HPK1) stress response signaling
 RT pathway activates I-kappaB kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of I-kappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I-kappaB/NF-kappaB system: a key determinant of mucosal
 RT inflammation and protection";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: WHILE IT IS EXPRESSED UBICITOUSLY THROUGHOUT
 CC THE MOUSE EMBRYO, AT E9.5 DAY ITS EXPRESSION BEGINS TO BE
 CC LOCALIZED TO THE BRAIN, NEURAL GANGLIA, NEURAL TUBE, AND IN LIVER
 CC AT E12.5 DAY. AT E15.5 DAY, THE EXPRESSION IS FURTHER RESTRICTED
 CC TO SPECIFIC TISSUES OF THE EMBRYO.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTO-PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
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 DR EMBL: AF026524; AAC23557.1; -;
 DR EMBL: AF088910; AAD52095.1; -;
 DR MGD: MGI:1338071; Ikbb.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 RV Phosphorylation.
 FT DOMAIN 15 300 PROTEIN_KINASE.
 FT DOMAIN 458 479 LEUCINE_ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 MEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 K -> D (IN REF. 2).
 FT CONFLICT 356 356 L -> F (IN REF. 2).
 FT CONFLICT 390 390 P -> Q (IN REF. 2).
 FT CONFLICT 406 406 K -> R (IN REF. 2).
 FT CONFLICT 573 573 TLMSTWLMDEERCSLEQACD -> VTA (IN REF. 2).
 FT CONFLICT 736 757
 SO SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;

Query Match 11.6%; Score 424.5; DB 1; Length 757;
 Best Local Similarity 22.3%; Pred. No. 5.8e-19;
 Matches 178; Conservative 121; Mismatches 302; Indels 197; Gaps 25;

OY 9 WHTDLLGOGATASVYKARNKSGELVAVVFNFTSYLRPREVOFEVILRKLNHNIY 68
 DB 15 WEMERLGTGGFNVIMHNOATGEQAIACQRELSPKRNKRCLEIQMLRNHNHNV 74
 OY 69 KLFVVE-----TGSRKQVLYMEYCGSSGLSYLESPEAFGLPEDEFLVLCVAGNM 124
 DB 75 AARDVPGMONLAPNDIPLAMEYCOGGDRLRYLNDPENCRCGREGAVITLLDIDIASLR 134
 OY 125 HLRNGIVHRDIPKGNIMRLVGEQSGISYKLTDFGARELDDDEKFEVYVTEGYLHPDM 184
 DB 135 YLHNRIIHRDLKRENIVLQGGKRLIKHIIIDGAKLEDQSLCTSEVGTIQYLAPEL 193
 OY 185 YERAVLKPQOKAGVYVDLMSIGVILYNAATGSLPPIPGGR-----RRNKETMYRI 237
 DB 194 LE-----QOKTYVDVMSFETLAFECITGFREFLPMMQPVQWMSKVRKSEVDIV 245
 OY 238 TTEPKAGIAGQRENGSPLEMSYTLPTQSLGLOSLVPLANTILE--VEQACW-- 293
 DB 246 SEDL-----NGAVKSSSLP-----PPNNINSLVARELKEWQLMDLMDMP 285
 OY 294 -----GDFQFAETSDILQRYVNVHFSLSQAVLHNTIYIHAHTIAIFQEAHKTQS 344
 DB 286 RQKGTDPQYGPNGCFRALDILMLKLVHVMVTGTVHPTVEDSLQSLKRIQENTG 345
 OY 345 VAPRHQVLEFEGHLCVLEPSVSAQHTAHTASSPLT-----PSTALPKGL 390
 DB 346 ILTDELLOKAGLVLLPKPAQCISDSTNGTLTMDLVFLDLSNKINETQTP-- 403
 OY 391 AFRDPAIDVPEKPYVDLQADYNTARGVAGAGYQALRLARALLDQELMFRGLHWMEVL 450
 DB 404 --RPPESSVCIQEPKRNISFQPLAKVAGVWHSI-----QTL 440
 OY 451 QATCRITLEVARTSLYL-----SSSLGTERFSSVAGTEPILQELKA----- 491
 DB 441 KEDCNRLQOGORAMMSLLRNNSCISKNNAMAST--AQOLAKKIDFFKTSIQIDLEK 498
 OY 492 -----AAELSRRLTALVLSRCSQ-----NITEQES----- 519
 DB 499 EOTERGITSDKLLANREMEQAVEQGRNDYKHLVERMALQTDIVDQSRPMGRKQGG 558
 OY 520 ----LSSLNRELV-----KSRQVHEDRS-----IQIQCCLDKMNITYQFKSRMR 563
 DB 559 TLDLDEQARLEYRLKREKPRDQRTGDSQEWVRLLLAQIQSEFKKVRITYQLSKT--- 615
 OY 564 PGIGVNEQDIIHLDKVNSHLAKRLQLQVQECVQKYOASLTVHGKRMVYHETRNHRL 623

DB 616 --VYCKQKALELPPV-----EEVY-----SLNEDERTVRLQEKRKEL 654
 OY 624 VCGSVACNT---EAQGVDSLSKLELSH--QLQDRAKGAQASPPIAPVSPTRKD 678
 DB 655 WMLKTIACSKVRQPGSPDSMN--VSRLSHPOQLMSQPSNACDS-----LRESKKSRE 707
 OY 679 LLLHMDLGCMMKLMSD 696
 DB 708 LVAEAHALCSRLSALQD 725

RESULT 4
 ID IKKB_HUMAN STANDARD; PRT; 756 AA.
 AC 014920; 075327;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1-)
 DE (I-kappa-B kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.,
 RT "IKK-1 and IKK-2: cytokine-activated I-kappaB kinases essential for
 RT NF-kappaB activation.",
 RL Science 278:860-866(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RC TISSUE=Heart;
 RX MEDLINE=98008814; PubMed=9346485;
 RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.,
 RT "I-kappaB kinase-beta: NF-kappaB activation and complex formation with
 RT I-kappaB kinase-alpha and NIK.",
 RL Science 278:866-869(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=99032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.,
 RT "I-kappaB kinase alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes.",
 RL Science 222:31-40(1998).
 RN [4]
 RP SEQUENCE FROM N.A., AND GENE MAPPING.
 RC TISSUE=Lung;
 RX MEDLINE=98438415; PubMed=9763654;
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.,
 RT "Assignment of I-kappaB kinase beta (IKKB) to human chromosome band
 RT 8p12->p11 by in situ hybridization.",
 RL Cytogenet. Cell Genet. 82:32-33(1998).
 RN [5]
 RP SEQUENCE OF 1-256 FROM N.A.
 RC TISSUE=Lung;
 RX Strausberg R.,
 RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.,
 RT "Coordinate regulation of I-kappaB kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.",
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [7]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;

RT			
FT	"The I kpa B/NF-kappa B system: a key determinant of		
RJ	mucosal inflammation and protection.";		
RL	Am. J. Physiol.	278:C451-C462(2000).	
CC	-I FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO		
CC	THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND		
CC	ULTIMATELY THE DEGRADATION OF THE INHIBITOR.		
CC	-I SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT		
CC	ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/MEMO.		
CC	HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN		
CC	ALSO BIND TO MEKK1, MAP3K14/NIK, IKAP AND IKB-ALPHA-P65-P50		
CC	COMPLEX. PHOSPHORYLATED IKB-ALPHA IS FURTHER RELEASED FROM THE		
CC	COMPLEX.		
CC	-I SUBCELLULAR LOCATION: Cytoplasmic.		
CC	-I TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, PLACENTA, SKELETAL		
CC	MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, TESTIS AND		
CC	PERIPHERAL BLOOD.		
CC	-I PTM: PHOSPHORYLATED BY MEKK1 AND PROBABLY ALSO BY MAP3K14/NIK.		
CC	WEAKLY AUTOPHOSPHORYLATED.		
CC	-I SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	IKAPPAB KINASE SUBFAMILY.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb.sib.ch).		
CC	-----		
DR	EMBL; AF029684; AAC51860.1; -		
DR	EMBL; AF080158; AAD08997.1; -		
DR	EMBL; AF031416; AAC64675.1; -		
DR	EMBL; BC006231; AAH06231.1; -		
DR	MTM; 603258; -		
DR	InterPro: IPR00719; Euk_pkinase.		
DR	InterPro: IPR002290; Ser_thr_pkinase.		
DR	InterPro: IPR001245; Tyr_pkinase.		
DR	Pfam: PF00069; pkinase; 1.		
DR	Pfam: PR00240; ubiquitin1.1.		
DR	PRINTS; PR00109; TYRKINASE.		
DR	SMART; SM00220; S_TKC; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
DR	PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.		
KW	transferase; Serine/threonine-protein kinase; ATP-binding;		
KW	phosphorylation.		
FT	DOMAIN	15	300
FT	DNAIN	458	479
FT	DOMAIN	737	742
FT	NP_BIND	21	29
FT	BINDING	44	44
FT	ACT_SITE	145	145
FT	MOD_RES	23	23
FT	MOD_RES	177	177
FT	MOD_RES	181	181
FT	MUTAGEN	44	44
FT			
FT	MUTAGEN	177	177
FT	MUTAGEN	177	177
FT	MUTAGEN	181	181
FT	MUTAGEN	231	256
FT	CONFLICT		
FT	CONFLICT	425	425
SQ	SEQUENCE	756 AA; 86563 MM; PGCADN671AAE91AE CMC61; O -> G (IN REF. 1). G -> H (IN REF. 5).	

Query Match	11.58;	Score 424;	DB 1;	Length 756;
Best Local Similarity	23.28;	Pred. No. 6.2e-19;		
Matches 181;	Conservative 123;	Mismatches 325;	Indels 150;	Gaps 0

9 WHTDLLGGCATISYKARKRKSGELVAVKYNFTTISLRPEVQVREFVLAKTKNHNLY 688
 | : || : : |:::| : : |
 | : || : : |:::| : : |

Db	15	MEKMERLGTCGFCGNVLRIMNHQETGEQIALKQCRQELSPRNRBRMCLEIQIMRSLFTHBNV	74
OY	69	KLPAVEE-----TGGSKQVLYMBEYCGSSGLSVLSBPENATGRLPDEFTLVVLCVYAGCN	124
Db	75	AARVPEGMOMNLAPNDLPPLAMEYCCGGDLKRYLWQFENCCGLRGALITLLSDIASALR	134
OY	125	HLRNGVLVHNDIAPGNIMRLVYEEGOSIYKLNDFGARELDDDEKFVSVYTEEYLPDM	184
Db	135	YLHENRLLIHNDLRPENIVLQGGQ-RLHKIIDLGAKELDDGSLCTSFVOTIQYAPL	193
OY	185	YERAVLRPOOKAFGVTVLMDISIGVTLVHAATGSLPFIPEGSP-----RRIMEIMYRI	237
Db	194	LE-----OQYTVLVDSVSEGTAFECITGTFREPLFMOPVOMHSHKVRKQSEVDIV	245
OY	238	TTKPRAGALAGQORENGRELEMYSTLPITCOLSIGLQSLQVPLILNILEVDAQ-----C	292
Db	246	SEDL-----NGYKFESSLPEPNNILSVLAELKEMWLOLMLMHPHQBGDP	293
OY	293	WGFDQFAETSDILQRYVVHVFSLQAVLHNITYHAANTIAIFQEAHVKQTSVAPRHOEY	352
Db	294	YGPNGCFKALDDITLKLTVILNMVGTIHTYVTEDESIGSLKARIODDGTGPEEDDEL	353
OY	353	LPEGLCYLPEBSVAQHIA-----HTTASPLTLESTA-----IPKGLA--	391
Db	354	LOEGLALIPDKPATQCSIDGKLINEGHTLDMDLVLEFDSKITYETQISPRQPEVSCI	413
OY	392	FDDPALDPKE-VKRV-----DLQADYTNAKCVILAGYQALRLKALLDGOELMR	441
Db	414	IQEPRLNIAFQOLKRWGQVHNSIQTLKECCNLO-----QGGAAAMNLLRNNSCTS	466
OY	442	GLHWMEVLYQATCRRLTEVARTSLIYSSLSGTERS-----SVAGTPET---QELKAA	493
Db	467	KKNKSMASMSOOLAKAKIDFFETSI-----OIDEKYSQETEGTISDKLLAMREDAV	521
OY	494	ELRSR--LRLTFLAVLNSCONITETQES-----LSSLRLRELV-----KSRDQ	533
Db	522	ELCGENEYKLLVERMALQTDIYDLORSFMKRGKQGTDLDDLEQARELYRLRREKPRDQ	581
OY	534	VHEDRS-----IQQIQCCLDKKNFTYQFKKSRMRPGLGTYNEQDIHKLDKVNFSHLAK	586
Db	582	RTEGDSQEMVRLILQALDISFEKKRVRIYTOLSKT-----VVCOKMATELPPKV-----	629
OY	587	RLQYFOFECYQKQASLYTHGKRMRYVHEHRLRLVYGSVAACNT---EAQGOEUS	643
Db	630	-----BEVV-----SLMNEDEKTVVRLQCRKOKELMNLKIACSKVGSPVSGSPDSIN	677
OY	644	KILLEISHOLLDRKAGQAQSPRIAPYPSPTKRDLHLHMOELCEGMKLLASDLDDNNR	702
Db	678	ASRLSQPGQLMSPSTASNS-----LDEPAKSPSELVAEHAHNC---TLENAIDQTVR	728
RESULT 5			
IKKB_RAT	STANDARD:	PRT:	757 AA.
AC	09078;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)		
DE	(1) (IKKB) (Nuclear factor (kappa-B) kinase beta) (IKK-B) (I-kappa-B kinase		
DE	2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBKB)		
GN	IKKB OR IKKBK.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RP	SEQUENCE FROM N.A.		
RA	Zhang Y., Sun S., Ravid K.;		
RL	"Ikk beta in megakaryocyte differentiation.";		
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.		
RP	[2]		
RP	IKK PHOSPHORYLATION.		

RA MEDLINE-99038238; PubMed-9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of Ikappa kinases by mitogen-activated protein
 RT kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [3]
 RP REVIEW
 RX MEDLINE-20178139; PubMed-10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:G451-G462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAPK14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAPK14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF115282; AAF21978.1;
 DR InterPro: IPR000719; Euk.pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKC_1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP: FALSE_NEG.
 DR PROSITE: PS00011; PROTEIN KINASE_DOM: 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST: 1.
 DR Transfaser: Serine/threonine-protein kinase; ATP-binding;
 KW phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 757 AA; 86866 MW; 3AFPE6A7DF91F9C CRC64;

Query Match 11.3%; Score 414.5; DB 1; Length 757;
 Best Local Similarity 22.4%; Pred. No. 2,4e-18;
 Matches 179; Conservative 118; Mismatches 304; Indels 197; Gaps 24;

QY 9 WHTDLLGGCATASYKANKKSGELVAVKVNNTSYLRPREVQVREPEVLKLNHONTV 68
 DB 15 WEMKEKLTGTGGGVNIRWNYQTGEOLAKOCROELSPKRNRCLEIQIMRLNHPNV 74
 QY 69 KLFAYEE---TGSRQKLVYVEYSSGSLVLESSENAEGLPEDEFLVLYRCVAAQMN 124
 DB 75 AARDVPEGNQNLAPRDLPLAMEYCOGGDLRRYLNQFENCGGLRGALITLLSDIASLR 134
 QY 125 HIRENGIYHRIKPGNIMLVEGEGSYIKLDFGARELDDDEKFEVSVEYGEETLHPDM 184

DB 135 YLHNRITIHDDIKPENIVLQOGEK-RLIKHTIDLGAKELDQSGICTSFVGLQYLAPEL 193
 QY 185 YERAVLRRKPOQKAFGVTVDLMSIGVTLVYHAATGSLPFIPFGG-----RRNKETMYRI 237
 DB 194 LE-----QOKYTVTVDPWVSFGTLAFECITGFREFRLNMQDPVCHSKVNRKQSEVDIV 245
 QY 238 TTEKPPAGALINGAQRRENGPLEMSTYLPITCOQLSGLSQSLVPLLANILEEQAK-----C 292
 DB 246 SEDL-----NGYVKESSSPFPNNNSVLAERLEKWLQIMLWQPRQSGVDPRQ 293
 QY 293 WGFDFEFAETSDILQRVVVFSLQAVLHHTYIHANHTALFOEAVHQTQSVARRHQEY 352
 DB 294 YGPNNGEFRALDILANKLVHILMTYGTHTHPVWEDESLQSLKTRIRREDTGLTDEL 353
 QY 353 LEFGHLCVLEPVSVAQHIAHTTASPLTL-----FSTAI-----PGLAFR 393
 DB 354 LQAGLVLLPDKPATOCISDSKTNEGTLTMDLVFLFDSKMSYEQITPRQPSVSC- 412
 QY 394 DPALDVPKFPKVDLQADVNTAKGVLAGQYQALRLARALLDQELMFGLIH-VNEVLDQ 452
 DB 413 --VLOEPK-----RNLSEFQMKRVGWGVHSTOTLKE 442
 QY 453 TCRRTLEVARTSILYL--SSLSGTERESSVAGTPEIOELKAAEL----- 495
 DB 443 DCNRLQGGGRALAMNMLRNNSCLSKMKKNMAST--AQQLAKLDFPKTSIQIDLEKYEQ 500
 QY 496 -----RSRLRTLAELVLSRCSONITETQES----- 519
 DB 501 TEEGITSKLLAMRMEQAVQCGRENDVYKVERMALQTDIVLDQSPMGRKQGT 560
 QY 520 --LSSLNRELY-----KSRDQVHEDS-----TQQLQCCLDKNFTYKQPKSKRRAPG 565
 DB 561 DDELEQARLYRLKREKPRDQTEGDSQDMVRLDQALQSFEEKRVLYLSQLSKT----- 615
 QY 566 LQYNEBQHKDKDYNFSLAKRLQLQVQECQYQASLVTHGRMRVYHTRNHLRYLG 625
 DB 616 VYCKOKALELLPKY-----EYVYR-----LNMDEKTYVRLQEKQKELMN 656
 QY 626 CSVAQNT---DAQVQPSLSKLELSHOLLQDRAKQAQASPPPTA---PYSPPTRKD 678
 DB 657 LTIKISKVGRFVSGSPSSMN--VSRISH-----PGLMSQPSACDSIPDSKSEE 707
 QY 679 LLHMQELCEGKLLASD 696
 DB 708 IYAEHAHLCSRLRESALQD 725

RESULT 6
 IKKA_MOUSE STANDARD; PRT; 745 AA.
 AC 060680; Q9D2X3;
 DT 16-OCT-2001 (Ref. 40, Created)
 DT 16-OCT-2001 (Ref. 40, Last sequence update)
 DT 16-OCT-2001 (Ref. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
 DE (I kappa-B kinase alpha) (IkBKA) (IKK-alpha) (IKK-A) (Ikappab kinase)
 DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBKA).
 GN IKKA OR CHUK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX STRAIN-BALB/C;
 RX MEDLINE-96044444; PubMed-7558004;
 RA Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
 RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
 RL chromosome 10 and mouse chromosome 19.";
 RN Genomics 27:348-351(1995).
 RP [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).

CC SPRAIN-PALB/C;
RX MEDLINE-96258427: PubMed-8777433:
RA Connolly M.A., Marcu K.B.;
RT "CHUK, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase
RT catalytic domain.";
RL Cell. Mol. Biol. Res. 41:537-549(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC SPRAIN-C57BL/6J: TISSUE=Colon;
RX MEDLINE-21085660: PubMed-11217851:
RA Kawai T., Shihagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akazawa T., Hara A., Furukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki T., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kodota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,
RA Schirral L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Doffell D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welfz C., Whitaker C., Wilmberg L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE-20198447: PubMed-10733566:
RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,
RA Gelezinas R., Marcu K.B.;
RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
RT IKKbeta have different activation requirements.";
RL Mol. Cell. Biol. 20:2635-2649(2000).
RN [5]
RP PHOSPHORYLATION BY MAP3K14/NIK.
RX MEDLINE-98188238: PubMed-9520401:
RA Nakanishi H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Okumura K.;
RT "Differential regulation of IkappaB kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [6]
RP IKKNA-IKKB BINDING.
RX MEDLINE-99212141: PubMed-10195894;
RA Delhasse M., Hayakawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of IkappaB kinase activity through
RT IKKbeta subunit phosphorylation.";
RL Science 284:309-313(1999).
RN [7]
RP IKK PHOSPHORYLATION.
RX MEDLINE-99038238: PubMed-9819420;
RA Nemoto S., Didonato J.A., Lin A.;
RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [8]
RP REVIEW.
RX MEDLINE-20178139: PubMed-10712233;
RA "Jabin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of
RT mucosal inflammation and protection.";
CC Am. J. Physiol. 278:CA51-CA62(2000).
-1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.

Db 135 LHENKIIHRDLKPNENIV-LADVGKGTIKHIIIDLGAKVDGSGICTSEVGTLOYLAPLELF 193
 QY 186 ERAVLRRKPOKAFGVTVLMSIGVTLVYHATGSLPEI-----PFGPRNRKIMRITTEK 241
 Db 194 E-----NRPYATVTVYNSFGIMVFCITIGYRPFLLHLOPFWEHEKIK-----KK 237
 QY 242 PAGAIAGQRRRBNGLPMSYTLF---ITQQLSLGLOSOLVYTLAN-----ILEVE 288
 Db 238 DPKCFACEEM-TGEVRRSSHLPQPNLSCLIVPEMSWQLMLNMPDQKGFIDLTIK 296
 QY 289 QAKCGFQFQFAEISDILQRRVYVNSQAVLHHIYTHANTAITQEAHVKQTSVAAR 348
 Db 297 QPRC-----FALMDHILNKIVHLNMTSAKISFLPCDESHLSQRIETRETIINTG 350
 QY 349 HOEYLFEGHLCVLPSPVSAQHIAHTTASSPLTFSTAIIPKGLARPDALDVPKRVYDL 408
 Db 351 SQELLSESGIS-LDP-----RKFA----- 368
 QY 409 QADVNTAKGVIGAGYQALRLARALLDQGLMFGHLMWMEVLAQTCHRTLE---VARTSL 465
 Db 369 -----SQCVLIDG-----VRGCDSYMVYLFDKSKTYVEGPFASRS-- 402
 QY 466 LYLSSIGTERESSVAGNPETIOELKAAELRSRLTAEVLSRCSQ----- 511
 Db 403 --LSDCVNYIVQDSKIQLPTIQLKVAEAVHYVSGLSKEYSRLQGOQRAMLSLRYNA 460
 QY 512 NITTOESLSSLNREL-----VKSQDVHEDRSIOQIOCC--DKMFTYKQFKSRMR 563
 Db 461 NLTKMKNTLLSASQOLKAKLEFFFRKSIOLEERYSEQMTYGISEKMLKMKMEEKAH 520
 QY 564 PG-----LGYNEEO-----IHKLDKYNFSLHAKRLLOVQOEVCVQYQ----- 601
 Db 521 YSEGVGVIEDQIMSLHTEIMELQKSPYRROGDMESLEQRAIDLYKOLKHPDPHLY 580
 QY 602 -----ASLVTH--GKMRVYHETRNHL-RLVGC-----SVAAQN-TEAGC-VQ 639
 Db 581 SDSTEMWKIIVHFVQSDRVILKELFGHLSKLLGCKOKIIDLKREVALSNIEADNTVM 640
 QY 640 ESLSKLEELSHOL-----LDDRAKGAQAS-----PPPIAPYSPFRKD 678
 Db 641 FMGKROKETWHLKIACTGSSAKSLVSSLEGTVPVPSAWMLPPLAD 689
 RESULT 7
 IKKA HUMAN STANDARD; PRT: 745 AA.
 AC 015111; 014666; Q13132; Q92467;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
 DE (I-kappa-B kinase alpha) (IKBA) (IKK-alpha) (IKK-A) (Ikkapab kinase)
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
 kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).
 GN IKKA OR CHUK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RC TISSUE=N-cell;
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
 RT "Identification and characterization of an Ikkapab kinase.";
 RL Cell 90:373-383(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=97394468; PubMed=9252186;
 RA Didonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
 RT "A cytokine-responsive Ikkapab kinase that activates the transcription
 factor NF-kappaB.";
 RL Nature 388:548-554(1997).

RN [3]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
 RP SER-176.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated Ikkapab kinases essential for
 NF-kappaB activation.";
 RL Science 278:860-866(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=99032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 RT "Ikkapab kinase-alpha and -beta genes are coexpressed in adult and
 embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RN [5]
 RP SEQUENCE OF 32-745 FROM N.A.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connolly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 families of interacting proteins, contains a serine-threonine kinase
 catalytic domain.";
 RL Cell. Mol. Biol. Res. 41:537-549(1995).
 RN [6]
 RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF S-176; T-179 AND
 RP S-180.
 RX MEDLINE=98188283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
 Ser-176.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 RN [7]
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RX MEDLINE=99413720; PubMed=10485710;
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt
 serine-threonine kinase.";
 RL Nature 401:82-85(1999).
 RN [8]
 RP IKKA-IKKB BINDING.
 RX MEDLINE=99212141; PubMed=10195894;
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of Ikkapab kinase activity through
 Ikbeta subunit phosphorylation.";
 RL Science 284:309-313(1999).
 RN [9]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [10]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED
 CC WHEN DEPHOSPHORYLATED.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT
 CC ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/IKK-
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50

CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- PTM: PHOSPHORYLATED BY MAPK14/NIK, AKT AND TO A LESSER EXTENT BY MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AF012890; AAC51662.1; -
 CC DR EMBL: AF009225; AAC51671.1; -
 CC DR EMBL: AF008157; AAD08996.1; -
 CC DR EMBL: U22512; AAC50713.1; -
 CC DR HSSP: P05132; IBRX.
 CC DR MIM: 600664; -
 CC DR InterPro: IPR000719; Euk_pkinase.
 CC DR InterPro: IPR002290; Ser_thr_kinase.
 CC DR Pfam: PF00069; pkinase.1.
 CC DR PRINTS: PR00109; TYRKINASE.
 CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 CC DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 CC KW Transphosphatase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
 CC FT DOMAIN 15 302 PROTEIN KINASE.
 CC FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).
 CC FT DOMAIN 738 743 NEMO-BINDING.
 CC FT NP_BIND 21 29 ATP (BY SIMILARITY).
 CC FT BINDING 44 44 ATP (BY SIMILARITY).
 CC FT ACT_SITE 144 144 BY SIMILARITY.
 CC FT MOD_RES 23 23 PHOSPHORYLATION (BY AKT).
 CC FT MUTAGEN 176 176 PHOSPHORYLATION (BY MAPK14).
 CC FT 23 T->A: LOSS OF PHOSPHORYLATION AND DECREASE OF KINASE ACTIVITY.
 CC FT 44 K->A: LOSS OF KINASE ACTIVITY.
 CC FT 44 K->M: LOSS OF AUTOPHOSPHORYLATION.
 CC FT 176 S->A: LOSS OF PHOSPHORYLATION AND OF ACTIVITY.
 CC FT 176 S->E: FULL ACTIVATION.
 CC FT 176 T->A: NO CHANGE IN PHOSPHORYLATION.
 CC FT 179 S->A: NO CHANGE IN PHOSPHORYLATION.
 CC FT 180 E->G (IN REF. 2).
 CC FT 543 L->R (IN REF. 5).
 CC FT 604 TS->A (IN REF. 5).
 CC FT 604 P->A (IN REF. 3 AND 5).
 CC FT 684 TS->DL (IN REF. 5).
 CC FT 687 TS->DL (IN REF. 5).
 CC FT 867 TS->DL (IN REF. 5).
 CC SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CAC64;
 QY Query Match 10.6%; Score 391; DB 1; Length 745;
 QY Best Local Similarity 23.0%; Pred. No. 6.7e-17;
 QY Matches 161; Conservative 116; Mismatches 300; Indels 122; Gaps 24;

DB 194 E-----NKRYTAVDVWVSFGTAVFECIAGYRPFLLHLOPFTWHEKIK-----KK 237
 QY 242 PAGATAGAGORRNGFLNLSYTLR---ITCQSLGQSOLVPLAN-----ILEVE 288
 DB 238 DKCFIFACEEM-SGEVRRSSHLQPNSLCSLIVERMNMIDLMWMDQORGQPVLDLTK 296
 QY 289 QAKCWGPFQFAETSDIILQRRVNVHFSLSQAVLHITYHANHTAIFQEAHVKNQSVAPR 348
 DB 297 QPRC-----FVLMHILMLKRVHLNMTSAKIIFLPPDESLSLDSRIEREIGITWG 350
 QY 349 HOEYLFEGHL-----CVLEP-----SVSAOHIAHTTASSPPLTFSTAPKGLA 391
 DB 351 SEELLSEFGISLIDPKRPAQSCVLDGVRGCDSTMYVLFPSKSTVEGPPASRSLSVCVNYI 410
 QY 392 FPDRLDVPKRF-VPRV-----DLQADYNTAKGVLAGYQALRLARALLDGOELMFR 441
 DB 411 VDSKTIQLPITQLRKVMAEVAHYVSGLEKEDYSRL-----FOGQRAAMLSL---LRYN 459
 QY 442 GLHWVNEVLQATCRRTLVARTSLYLSLSIGTERFSS--VAGTPEIQELKAAELNRL 499
 DB 460 ANLTMKKNTLLISASQOLK-AKLEFFHKSIQDLERYSPQNTYGISSEKMLAKMEKEKA 518
 QY 500 RFLAEVLSRCSONITETQESLNLRELKSRDQVHEDRSIQIQCCLDKNNITYKQFKK 559
 DB 519 IHYAEV-----GVIGYLEDQIMSLHAEIMELQKSPYGRQDLMESLQRAIDLYKOLKH 573
 QY 560 SMRRCG-LGYNEEQ-----IHKLD-----KVNSHAKKL-----LQVQOE 594
 DB 574 ---RPSDHSISDSTBMKVIYHTVQSDPRVLEKELGHSILKCLGCKOKIIDLIPVEVALS 630
 QY 595 BCQVKYQASLVTHGKRMVRVHETRNHLRVGCSYVACNT 633
 DB 631 NIKKADNTVMFQGRKQKEIM---HLKIKACTQSARS 665
 RESULT 8
 ID UKL1_MOUSE STANDARD; PRT; 1051 AA.
 AC 070405;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase UKL1 (EC 2.7.1.1) (Unc-51-like kinase 1) (Unc51.1 serine/threonine kinase).
 GN UKL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE-Brain.
 RP MEDLINE=98262945; PubMed=9600096;
 RX Tan U., Kuroyanagi H., Kuroiwa A., Matsuda Y., Tokumitsu H., Tomoda T., Shirasawa T., Muramatsu M.-A.;
 RT "Identification of mouse UKL1, a novel protein kinase structurally related to C. elegans UNC-51.";
 RL Biochem. Biophys. Res. Commun. 246:222-227(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20086285; PubMed=10624947;
 RA Tomoda T., Bhatt R.S., Kuroyanagi H., Shirasawa T., Hatter M.E.;
 RT "A mouse serine/threonine kinase homologous to C. elegans UNC51 functions in parallel fiber formation of cerebellar granule neurons.";
 RL Neuron 24:833-846(1999).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. APG1/UNC-51/DLK1 SUBFAMILY.
 CC -----
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CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; AF053756; AAC40118.1; -
DR EMBL; AF072370; AAF23317.1; -
DR HSSP; P00523; 2PTK.
DR MGD; MGI:1270126; Utk1.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 16 278 PROTEIN KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 46 46 ATP (BY SIMILARITY).
FT ACT_SITE 138 138 BY SIMILARITY.
FT DOMAIN 297 310 POLY-SER.
SQ SEQUENCE 1051 AA; 112462 MW; 998021985FBAE8A0 CRC64;

Query Match 8.3%; Score 305.5; DB 1; Length 1051;
Best Local Similarity 26.8%; Pred. No. 2e-11;
Matches 91; Conservative 52; Mismatches 127; Indels 69; Gaps 10;

QY 1 MOSTANYLMHDDLLGCGATASVYKARKKSGEL-VAVKVNTNTSYLRPREVOYREFEVL 59
DB 8 VETVGKFEFSRKDLIGHAFVVEFGRRKHDELVAAKCKNKKNLAKSOTLLGKEIKIL 67
QY 60 KRLNHNIVKLFVAEETGSGROKVLVMEYCGSSGLSVLESPENAFGLPEDEFLVLRGV 119
DB 68 KELKHNIVKLFVAEETGSGROKVLVMEYCGSSGLSVLESPENAFGLPEDEFLVLRGV 119
QY 120 VAGMNLHRENGIVHNDIRPGNIMRLVGEEOGSI-----YKLTDFGARELDDDEKFPVS 173
DB 123 AGAMLLHSKGIIRHDLKPQNIL-LSNPGRRANPSIRVYKIDAFGRVYIQSNNMATL 181
QY 174 YGTEYLHPDMYERAVLKKPOOKAFGVTVLMSIGVLYHAATGSLPFIPEGGRRKKEI 233
DB 182 CGSPYMAPEVL-----MSQHYDGKADLMSIGTVYQGLTGKAPF-----QASSPQ 227
QY 234 MRRITTEPAGAIAGAOBRENGPLEWSTLPTTQOLSIGLOSQVPLIANTILEVEQAQKW 293
DB 228 DLRLFEYENKTLVPIPIRETSAPLR-----QLLAL-----LQRNHRDM 267
QY 294 GPDFFAETSILORVVVHVESLSQAVLHNTIYHAHNTI 332
DB 268 DDEFF-----HHFFLDASPI 284

RESULT 9
UTK1_HUMAN STANDARD; PRT: 1050 AA.
ID UTK1_HUMAN
AC 075385;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase Utk1 (EC 2.7.1.-) (Unc-51-like kinase
DE 1)
GN UTK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=98360094; PubMed=9693035;
RA Kuroyanaqi H., Yan J., Seki N., Yamanouchi Y., Suzuki Y.-I.,
RA Takano T., Muramatsu M.-A., Takasawa T.;
RT "Human Utk1, a novel serine/threonine kinase related to UNC-51 kinase
RT of Caenorhabditis elegans: cDNA cloning, expression, and chromosomal
RT assignment.";
RL Genomics 51:76-85(1998).
CC -1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED. DETECTED IN THE
CC FOLLOWING ADULT TISSUES; SKELETAL MUSCLE, HEART, PANCREAS, BRAIN,
CC PLACENTA, LIVER, KIDNEY, AND LUNG.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC APG1/UNC-51/UTK1 SUBFAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL; AF045458; AAC32326.1; -
DR HSSP; P00523; 2PTK.
DR MTM; 603168; -
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR002290; Ser_thr_Pkinase.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 16 278 PROTEIN KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 46 46 ATP (BY SIMILARITY).
FT ACT_SITE 138 138 BY SIMILARITY.
FT DOMAIN 297 310 POLY-SER.
SQ SEQUENCE 1050 AA; 112601 MW; 4ED9B94028E3C138 CRC64;

Query Match 8.3%; Score 303.5; DB 1; Length 1050;
Best Local Similarity 27.2%; Pred. No. 2.6e-11;
Matches 92; Conservative 53; Mismatches 124; Indels 69; Gaps 11;

QY 2 QSTANYLMHDDLLGCGATASVYKARKKSGEL-VAVKVNTNTSYLRPREVOYREFEVL 60
DB 9 EYVGKFEFSRKDLIGHAFVVEFGRRKHDELVAAKCKNKKNLAKSOTLLGKEIKIL 68
QY 61 KRLNHNIVKLFVAEETGSGROKVLVMEYCGSSGLSVLESPENAFGLPEDEFLVLRGV 120
DB 69 ELKHNIVKLFVAEETGSGROKVLVMEYCGSSGLSVLESPENAFGLPEDEFLVLRGV 120
QY 121 AGMNLHRENGIVHNDIRPGNIMRLVGEEOGSI-----YKLTDFGARELDDDEKFPVS 174
DB 124 GAMLHSHKGIIRHDLKPQNIL-LSNPGRRANPSIRVYKIDAFGRVYIQSNNMATL 182
QY 175 GTEYLHPDMYERAVLKKPOOKAFGVTVLMSIGVLYHAATGSLPFIPEGGRRKKEI 234
DB 183 GSPYMAPEVL-----MSQHYDGKADLMSIGTVYQGLTGKAPF-----QASSPQ 228
QY 235 YRITTEPAGAIAGAOBRENGPLEWSTLPTTQOLSIGLOSQVPLIANTILEVEQAQKW 294
DB 229 DLRLFEYENKTLVPIPIRETSAPLR-----QLLAL-----LQRNHRDM 268
QY 295 FDOFFAETSILORVVVHVESLSQAVLHNTIYHAHNTI 332
DB 269 DDEFF-----HHFFLDASPI 284

RESULT 10
UTK1_HUMAN
Y537_HUMAN

ID Y537_HUMAN STANDARD; PRT; 661 AA.
AC 060285;
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Probable serine/threonine-protein kinase KIAA0537 (EC 2.7.1.-).
GN KIAA0537.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kicani H.,
RA Nomura N., Ohara O.,
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.",
RL DNA Res. 5:31-39(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB011109; BAA25463.1; -
DR HSSP: P00518; 1PHK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KM Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding.
FT DOMAIN 55 306 PROTEIN KINASE.
FT NF_BIND 61 69 ATP (BY SIMILARITY).
FT BINDING 84 84 ATP (BY SIMILARITY).
FT ACT_SITE 178 178 BY SIMILARITY.
SQ SEQUENCE 661 AA; 74304 MW; 806f37d52ca4718f CRC64;

Query Match 8.1%; Score 299; DB 1; Length 661;
Best Local Similarity 23.7%; Pred. No. 2.8e-11;

Matches 159; Conservative 116; Mismatches 250; Indels 146; Gaps 36;

OY 9 WHDDLLGCGATASYVYARKKKSGELVAVVFNTSTLRREYQ---REPEVLRKLNQ 65
DB 55 YEIQETLGKGYGVKATKRSRVAIKSIRKDK- IKEDQDMVAHRIKELISSLNHP 113
OY 66 NYVLFAVEETGSGSRK-VLWMEYCSGSLVLESPENAFGLPEDEFLVLRGVAGNM 124
DB 114 HILSIYEVEF---NKDAIIVIMEASGELXYDISERR---LSERCTRPFROIYSAVH 167
OY 125 HLENGIVHNDIKPKNIMRLVGEESQIYKLTDFGAARELDDDEKFEVSVY-GTEEYLAPD 183
DB 168 YCHNGVYHNRDLKLENTILL---DDNCNRIKIDFGLS-NLYQKDKFQJFCGSPLYASPE 222
OY 184 MYEAVLARKPKQKAFYTVLDMISGVLYHAAGCSLPEIFGGRKMKELM---YRTITE 240
DB 223 IVNCRPYRGPE---VDSWALGVLLYLYLVGTMPFDGDKNKLIRQLISSGGEYRPTQ 275
OY 241 KPAGA-----TAGAQR-----ENGLPWSYTLPTICOLSLG-AGSOLVPILANIL 285
DB 276 -PSDARGLIRKMLAVNDRATIEDIANHHMVMVNGYSSV-CCDD-A-HHSESLARII 332

OY 286 EVE-----OAKCWGDFQFAETSDIL---QRVWVHPSLSQAVLHHTIHAHNTI 332
DB 333 DMHNNHSTGADTPEAKMKMLAK--PTTSEVMELRQ-----SLKSKKNEF--AQSGQ 382
OY 333 AIFQEAHVKQTSVADPHQOYLFEGHLCVLEPVSQAQHIAHTTA-----SSPLT--- 380
DB 383 DAVPESPSTLSSKRPKG-----ILKRSNSEHRSHTGFTGCVGPAIPSTFKME 432
OY 381 --LEFSAIRKGLAFNRDPAIDV-KFVPKYVDLQADVTAGVY-----GAGYQA---URL 428
DB 433 QDLCKTGV---LLPSPPEAEVPGKLSPK---OSATPPKGIILKTQQRSGSYSSPENSE 486
OY 429 ARALDDQELMERGL-----HWMEVLAQTCRRTLAEVARTSLYLSSSLGTE 475
DB 487 SSELDSNDVMSSTSPSPDPARYTSH-----SLSCR-----RKGIILKSSKYSAG 534
OY 476 RFSVAVGTEPIQELKAAALRSRLRLAVALVRSQONITETQESLSLNRELYKRDQVH 535
DB 535 TMDPALVSEMPLESLSEPCVPAEGLSRYSRPSVISD-DVSLSSDSFDL---DLQ 589
OY 536 EDR-STIOIQCCLDKNFTYKQ-FKSRMRPGIGVNEQIHKLDKYNFSLHAKRLLOYRQ 593
DB 590 ENRPANQIRSCVSAENFLQIDFEGLONRPRQYLKRYRNLABDSFSLTD-----M 643
OY 594 EECVQRYQASL 604
DB 644 DQVTVYKQAL 654

RESULT 11

ID KP78_HUMAN STANDARD; PRT; 713 AA.
AC P27448;
DT 01-AUG-1992 (rel. 23, Created)
DT 01-AUG-1992 (rel. 23, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Putative serine/threonine-protein kinase p78 (EC 2.7.1.-).
GN p78.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maheshwari K.K., Som S., Parsa I.;
RL Submitted (JAN-1992) to the EMBL/Genbank/DBJ databases.
CC -1- MISCELLANEOUS: MARKER PROTEIN LOST IN CHEMICALLY INDUCED
CC TRANSPLANTABLE CARCINOMA AND PRIMARY CARCINOMA OF HUMAN PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC NIM1 SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M80359; AAA59991.1; -
DR PIR: S27966; S27966.
DR HSSP: P00518; 1PHK.
DR MIM: 602678; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR001772; KAL.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR000449; UBA.
DR Pfam: PF02149; KAL; 1.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00627; UBA; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00165; UBA; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

RESULT 12		
GIN4_YEAST	STANDARD;	PRT: 1142 AA
ID GIN4_YEAST		
AC Q12263;		
DT 01-NOV-1997	(Rel. 35, Created)	
DT 01-NOV-1997	(Rel. 35, Last sequence update)	

[illegible]

QY 227 -----PRNKEIMYRITTEKPA-----GATAGAO 250
 DB 240 TLLKXQKGFEMPSDELSREKODLIRKILYDPERIRKTRDKLHFLQKPSIRDSK 299
 QY 251 RRENGPLEMSTYLPITCOLSLGLOSLVPLANILEVEAKW-----GFDQFAETSD 304
 DB 300 SINGLPREDYTLPR-----LSESNSSIDATLQMLVIL-----WGRDPEGKIKLEKPEGA 350
 QY 305 ILQRYVHVH-----SLSQAVLHHIYIAHNTAIFQEAHVKOTSAV-----RHQOELFES 356
 DB 351 NAKRTYALLYRRKCDTOKELIKOQVKKQSSISVSFSSKVSSTPQRRRRESLISY 410
 QY 357 HLCVLEPSYAOHIAHTTASSPLTL-----FSTAL-----PKGLAFRD 394
 DB 411 TSSRRKPISNKFTASASSNLTTEGSSKRLSKNFSSKKLSTYVQSSPTASRNKRA 470
 QY 395 PALDVPKVPKVLQADYNTAKVGLAGYQALALA-----RALDQGLMFRGL 443
 DB 471 SVINVERKOKRASI-----FSTYKKKRSRSIKHMSLIPSKRBSVTYTKLMSTYAKLAEDD 527
 QY 444 HWMEVLOATCRPLEVARTSLYLSSLSGT-----ERFSSVAGTPE-----IOELK 490
 DB 528 DW-ETIEKETKRT-----SSNFATLIDELFEYKYEIOIRKIKKELEKRYEAK 574
 QY 491 AAEL-----RSRLRTLAEVLNRCSONITETQESL-----SSLNRELVSROQ 533
 DB 575 ARELEHRRRRKOEKERARLLE-----KEDLKRKQELAKKQJEDISDELEQELSKHEE 629
 QY 534 -----VHERSIOQIOCCLD-----KMFYIKQPKSRMRPGLYNE--EQH 574
 DB 630 KLDGNISISAPMENEKKNHLEVDIDNLLRRNFSLQRPVSLDQIMFSSPTEVS 689
 QY 575 KLDKNFSH-----LAKRLVFOEEOCYOAYASLVTHGKRRM-----VWETRNHL 621
 DB 690 PVKRRKRENEMLTEKKILETIR-----SKFLGSSFNIDKELKSKMEPSLIAQRISEE 746
 QY 622 RLVGCSVAACNTEAGVOESLSKLELSHOLLDRAKKGAQASPPPLAP-----Y 671
 DB 747 RVV-----SDSNDGYESL--TLPRKDGNGVQ--LKDSATATAPVSDGRKISEIRV 794
 QY 672 PSPTRKDLLHMOELCGMKLLAS-----DLLDNRI-----IERLRVAP 713
 DB 795 POFTRKS--RHFSKSKRLSVLSMTKESFTNLVDILKGNLDVNNQOSORITP 848

RESULT 13
 ST10_MOUSE STANDARD; PRT; 966 AA.
 ID ST10_MOUSE
 AC 05096;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase 10 (Ec 2.7.1.37) (Lymphocyte-oriented kinase).
 GN STR10 OR LOK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=97426413; PubMed=92784426;
 RA Kuramochi S., Moriguchi T., Kuida K., Endo J., Semba K., Nishida E., Karasuyama H.;
 RA "LOK is a novel mouse STE20-like protein kinase that is expressed predominantly in lymphocytes";
 RL J. Biol. Chem. 272:22679-22684(1997).
 CC -1- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND HISTONE H1A ON SERINE AND THREONINE RESIDUES.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS

CC SUCH AS SPLEEN, THYMUS, AND BONE MARROW.
 CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC STE20 SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: D89728; BAA24073.1; -
 DR HSSP: P24941; ICRP.
 DR MGD: MGI:1099439; STK10.
 DR InterPro: IPR000719; Euk.pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; Coiled coil.
 KW DOMAIN 36 294 PROTEIN KINASE.
 FT DOMAIN 588 936 COILED COIL (POTENTIAL).
 FT DOMAIN 749 883 GLN-RICH.
 FT NP_BIND 42 50 ATP (BY SIMILARITY).
 FT BINDING 65 65 ATP (BY SIMILARITY).
 FT ACT_SITE 157 157 BY SIMILARITY.
 SQ SEQUENCE 966 AA; 111992 MW; 7115EAC01032BF94 CMC64;

Query Match 7.8%; Score 286; DB 1; Length 966;
 Best Local Similarity 22.1%; Pred. No. 2.9e-10;
 Matches 186; Conservative 122; Mismatches 314; Indels 220; Gaps 37;

QY 6 NYLMTDDLLGCAATASVYKARKKSGELVAVYFNTSTLRPREVQVREFYLRKLNQ 65
 DB 33 NDWEIYVGLDGFAGFYVAKKNGKGTALAAVIEFKS--EELEDYIVEIELATGCDHP 91
 QY 66 NYKLFVVEETGSGROKLVN--EYCSGSLVLESPENAFGLPEDDFVLRCVAGNN 124
 DB 92 YIVKLLGATYYDG---KLMIMIEFCGAVDAIMLEDR--GLTEQIQVYVCOMLEALN 146
 QY 125 HLRENGIVHRDIRPGNI--MRLVGEEGOSIYKLTDFG--AAELDDDEKVSYSVEEYLRP 182
 DB 147 FLHGKRIIHRDLKAGNVLMTLEGD-----IRLDPGVSANKLTKQKDSICTPYWMAP 201
 QY 183 DMERAVLRKRPQOKA--FGVTVVDLMSIGVLYLHAATGSLPRTIPGGRPKRKEIMRTTEK 241
 DB 202 EV---VLCTMDADAPDYKADIMSLGITILEMAQEPRIHED--NPWR--VLLKTKASD 253
 QY 242 PAGALAGQRRNGPLMESTYLPITCOLSLGLOSLVPLANILE----- 286
 DB 254 PPTLLT-----PSKWSYEFDFELKIALDKNPETPSAQLQHPFVSRYTSNKALRE 305
 QY 287 -VEQAKMGFDQF-----FAETSDILQRYVHVHVSLSQAVLHHIYIAHNTAIFQEAHV 340
 DB 306 LVAEAKAEVMEIEDGREDDEEDAVDAV-----PPLVNHQDSANVTQPSLSNKL 357
 QY 341 KQTSVAPRHQEYLFEGHLCVLEPSVSNQHT-----AHTTASPLTLFSTALPRGLAFRDP 396
 DB 358 LQDSSTP-----LPSQPOEPVNGPCSPSGGCPLOTTSFA--DGLSKNDND 402
 QY 397 LDVP-----KFPVKVLQADYNTAKVGLAGYQALRALALDQ 436
 DB 403 LKVPVPLKRSRPLSMARIQMDKEKQIPDDDENSPSAKSGRANGSRPSSALETLGGE 462
 QY 437 ELMFRLHWMVEVLOATCRPLEVAR-----TSL---LYLSSLSG----- 473
 DB 463 ALTNGLELSSVSPSHSKRASDCSNLSTESMDYGTSLADSLANKETSLSLKSGSLH 522

QY 474 -----TERF-----SSVAG-----TPETIOEIKAAELRSRLRT-- 501
 Db 523 NNTLKTRRFVVDGVEVSTTSITSEDEKDEMEFLRQRLRELRLLQKFEHNRQTL 582
 QY 502 -----LAEVLSRCSONTTEOE-----SLSSINRELVSRQVNEHDSIQOICCLDM 550
 Db 583 SSKHEQLQOMKRRFEOELINAKKFFDVLEMLEKQKQVVKEMODHSVRR----- 634
 QY 551 NTIYQFKFSRMRPGILGYN-EEQIHKLDKVNSHLAKRLLOVFEQCYQKQASLYTHG 608
 Db 635 ---KEBAKRIELEODRDYAKFOELKQMKKEVSEVEKLPQQRRESKQKME-----EHS 687
 QY 609 -KRMRY-----VHETRNHLRLVGCSSVA-----CMTBAQVOESLSKLEISLHOLLDR 657
 Db 688 OKQQRDRDFVAKQKEDLELARKLTTENRREICDKE-----RDCLSK-----KQELLDR 738
 QY 658 AKGAQAPPIAPSPPTKDLLHMOELCEGMKLASLDD-----NNRIIE 705
 Db 739 -----EALWEMEHQLOERHOLV--KQQLKQYFLQRHDLRKHEKEREMORYNOME 792
 QY 706 RL 707
 Db 793 QL 794

RESULT 14
 YNH4-CAEEL STANDARD; PRT; 863 AA.
 AC P32742; P32741;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Putative serine/threonine-protein kinase R107.4 in chromosome III
 (EC 2.7.1.-).
 GN R107.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdittida; Rhabdicoidea;
 OC Rhabdittidae; Peloderinae; Caenorhabdittis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnesough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Crexton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifen C., Rofpra A., Saunders D., Shownkeen R.,
 RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Stuston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Wohldman P.;
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: Z14092; CAA78473.1; -
 DR PIR: S30874; S30874.
 DR WormPep: R107.4; CE03579.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.

DR Pfam: PF00069; Pkinase; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Hypothetical protein; transferase; serine/threonine-protein kinase;
 KW ATP-binding.
 FT DOMAIN 57 335
 FT NP_BIND 63 71
 FT BINDING 85 85
 FT ACT_SITE 185 185
 FT ACT_SITE 185 185
 FT BY SIMILARITY.
 SQ SEQUENCE 863 AA; 98701 MW; DA42D263CA4003F8 CRC64;

Query Match 7.8%; Score 285.5; DR 1; Length 863;
 Best Local Similarity 21.4%; Pred. No. 2.7e-10;
 Matches 168; Conservative 127; Mismatches 269; Indels 221; Gaps 37;

QY 7 YLWHTDDLQAGAVASYKARKNKSGELVAVKVFNTSYLRPREQVYR-----PEFYLRLK 62
 Db 55 YTLFNDSEIGKAGAYSEVYRGRT-ESGRVAVKT-----ACKKLEVAALGIEIETLKKL 106
 QY 63 -NHQNIYKFLAVETGSSROKV-----LYMEYSSGSLSLVLESPNMFGLPEDEFL-V 114
 Db 107 KGASNIYQYFGSNMTKMAPSVTSETISFAMEYASS-SLEAEMRRPKRNHGLSSNALIDL 165
 QY 115 VLRCVVGAMNHLRENGIVHDIKPGNIMRLV-----GEGSQSYKLTLDGCAARELDD-- 167
 Db 166 VVDCSMA-LSALREHNIAHNDIKHNNILFPGTPTGRNSTLFLKLDGCSKSLSENS 224
 QY 168 EKQVSYVTEERYLHP-----DMEYRAVLR-----KPOOKAFGVYVDMISIGVLYHAATGS 218
 Db 225 HEMTLYGTPLNLLPFLAHMEVDPLMAQNHNKTKSAVTSQCDLMAIGLTLPFCATK 284
 QY 219 LRFPGCGPRNKKEIMYR-----ITTEKPAGALAGAR-----RENPLKSTLPTPT--- 266
 Db 285 ---PPEHERNNKSLYHKAVALTONPDALAVLYKGDPCGRDIDFEQ---PVTLEP 338
 QY 267 ---QSLSLGLOSLVPLNILEVDAQKCGEPOFAERFSDILQRYVAVFSLSQAVLHH 323
 Db 339 AKFTRYPKMLVSTMTCLRSFFHEPSI-----EYAKAVADMARNKRRITFS----- 384
 QY 324 IYIHANTIAIPQAV--HKQTSVAPRHOBYLFEGLCVLEPSVSAQIHAHTTASPPLTL 381
 Db 385 -----SVDMQSLVEHTDMSNVP-----HLGFSIPSIS-KCLGYPEGDIDILL 425
 QY 382 FSTA-----IPKGLAFRDP--LDVPFVKKVLDADYNTAKGVLAGYQA 425
 Db 426 SNTSTHYLDSKQKSVGDLDTLVVPOISHVDMKILAR---NIEFHEPDMTRKLSE 482
 QY 426 LRLARALLDQELMFRGLHVMVEVLA--ATCRRTEVANTSLLYSSLSGT-ERFSSVA- 481
 Db 483 IRIKCC-----YGLSMLTEIDEYALFDRVSTILSTQSSLVQELSGFERQVTSR 534
 QY 482 -----GRIPE-----IQELKAAELRSRLRLAELVLSGSONTET 516
 Db 535 FAVYVMASVPLMLFDEANPEYKMTSDQIAKRRRELEHARVSMIDIECAQLSKD 594
 QY 517 QESLSINRELVKSRDQVH-----EDRSIQOICCLDKMNFYQFKFSMR 563
 Db 595 AEDLRLEDMDLDGICEISYVFYDQKALLSTQKTSQELVELCLRRNNIMQFNSP-- 652
 QY 564 PGLGYNEOIHKLDKVNSHLAK-----RLQVFEQECVQRYQASLYTHG 608
 Db 653 -----DRINKSKLKNKAMLAASLSQLSNRYKQLQDMISECVILLE----- 692
 QY 609 KRMRYVHERFN-HLRVYGSSVAACNTBAQVQ-----ESLSKLEELS 650
 Db 693 KPFQEKMDIVNNYLDAGGS---RMTQKSMHLRPFHESQIRIKTKTKSCRKLIDLN 749
 QY 651 HQLDQ 655
 Db 750 IELDQ 754

RESULT 15
APG1_YEAST

ID	STANDARD	PRT	897 AA
AC	P53104		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Autophagy serine/threonine-protein kinase APG1 (EC 2.7.1.-).		
GN	APG1 OR AUT3 OR YGL180W OR G1615.		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.		
OX	NCBI_TaxID=4932;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=5288C / F1679;		
RX	MEDLINE=97197971; PubMed=9046087;		
RA	Coglievina M., Klima R., Bertani I., Delneri D., Zaccaria P.,		
RA	Bruschl C.V.;		
RT	*Sequencing of a 40.5 kb fragment located on the left arm of		
RT	chromosome VII from Saccharomyces cerevisiae.*;		
RL	Yeast 13:55-64(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS.		
RC	STRAIN=X2180;		
RX	MEDLINE=97368130; PubMed=9224897;		
RA	Matsura A., Tsukada M., Wada Y., Ohsumi Y.;		
RT	*Applp, a novel protein kinase required for the autophagic process in		
RT	Saccharomyces cerevisiae.*;		
RL	Gene 192:245-250(1997).		
CC	-1- FUNCTION: PROTEIN KINASE THAT IS INVOLVED IN THE REGULATION OF THE		
CC	AUTOPHAGIC PROCESS, A PROTEIN DEGRADATION PROCESS. FOUND TO BE		
CC	ESSENTIAL FOR THE FORMATION OF AUTOPHAGOSOMES. REQUIRED FOR THE		
CC	MAINTENANCE OF CELL VIABILITY UNDER STARVATION.		
CC	-1- PTM: AUTOPHOSPHORYLATED. MAY BE REGULATED BY A SECOND PROTEIN		
CC	KINASE. THE PHOSPHORYLATION STATE MAY PLAY A ROLE IN THE INDUCTION		
CC	OF PROTEIN DEGRADATION UPON STARVATION.		
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	APG1/UNC-51/ULK1 SUBFAMILY.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; X91489; CAA62794.1; -		
DR	EMBL; Z72702; CAA96892.1; -		
DR	EMBL; D29991; BAA21481.1; -		
DR	HSSP; P24941; 1CKP.		
DR	SGD; S0003148; APG1.		
DR	InterPro: IPR000719; Euk_pkinase.		
DR	InterPro: IPR002290; Ser_thr_pkinase.		
DR	Pfam; PF00069; S_TKc; 1.		
DR	SMART; SM00220; S_TKc; 1.		
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE: PS00111; PROTEIN_KINASE_ST; 1.		
KW	Transferase; Serine/threonine-protein kinase; ATP-binding;		
KW	Phosphorylation; Autophagy.		
FT	DOMAIN 24 325		
FT	NP_BIND 30 38		
FT	BINDING 54 54		
FT	ACT_SITE 172 172		
FT	MUTAGEN 211 211		
FT	MUTAGEN 237 237		
SO	SEQUENCE 897 AA; 101717 MW; 7FAC785AA3A7CC46 CRC64;		

Query Match

7.6%; Score 281; DB 1; Length 897;

Best Local Similarity 20.2%; Pred. No. 5,3e-10;
Matches 177; Conservative 124; Mismatches 315; Indels 262; Gaps 34;

```

QY 1 MOSTANTYLMHDDLLGCGATASVYKAR-NKSGELVAAKVFNTSYLAPREVQVNEF-- 57
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 18 MASAAINYT--AEKEIGKGSFAFVYRGHLTSDKSGVAAIKESRAKLNKLLNLEIEIA 75
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 58 VLRKLNHGVYKLFVVEEFGSRQKLVVMEVCSGLSLVLE----- 99
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 76 ILKKIKHPIVILDCERT--STDVYLMEYCALDGLFLKRRKELMENNPLRTVEK 133
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 100 ---SEENAFGLPEDEFLVLRVAVGMNHLRENGIVHNDIRGNI----- 141
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 134 YPPSENNHGLHRAVFLSYLQALASAKFLRSKNLVHNDIKPQNLSTPLGYHDSKSF 193
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 142 ---MRLVGEESGIVYKLTDPGARELDDEKPVSVYSTEIEYLHPDM--VERAVLRKPOKA 197
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 194 HELGFEVGIYNPLIKTIADGFARFLPNTSLAETLGGSPLYMAPETLNYOK----- 243
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 198 FGVTVDLMSIGVLYHAATGSLPFIPIFGGPRRNKEIMRTTEKPAAGIAGNRRNGPL 257
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 244 YNAKADLMGVGVVEEMCGTPPF-----RASNHLLEPKI----- 286
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 258 EWSYLPITCQLSLGQSOLVPILANILEVEQAKCGEDQFPA----- 306
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 287 ---TFPSYC-----NIEPELKEILCSLLTFDPAORIGFEFFPAKVVNEDLSYELEDL 338
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 307 -----ORVVVHFSLSQAVLHILYHANT 331
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 339 PELESKSGIVSENMFSVYLSKQKSPNSNLAGHOSMDNDELSDAKNSNLTAAV 398
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 332 IAIPEAVHVKQTSVAPRHOEYL-----FEGHLCVLE-PSYSAOHIA----- 372
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 399 KRDHQVADVKKSNKYNHNSLYSDSFEFEYVVEKSEVNSLADYVAGQGFNPPIKH 458
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 373 TPAAS-----SPLTFSTALPKG-----LAERPALDVPK 401
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 459 PTSTONQVNLNEQSPNNQYFONQGENPRLRATSSSGSGSDGSRPSLYCDRLSTSS 518
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 402 FVPKVDLADVYTFAGVUL--GAGYOALR-----LARALLDGEELMVRGL--HWMEV 449
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 519 LNPSSNLSALDIASTRLEFGANQOQOQITSSPPYSOTLLNSQ--LEHLEITENILTI 576
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 450 LGATCRRTLEVARTSLYSSSLGTE-----RESSVAGTEPIQELKAAELRSRL 499
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 577 DHLQHPETLKLDNTNIVSLTESLAAKAFVVSVAEKKFSQI--VPLSTPLKGMAFENR- 633
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 500 RFLAEVLSKSONITETQSSLSLNRELYKSRDQVHEDRSIQI--QCCLDKKNFTYKQK 558
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 634 -----RSMDSNAIAEEDD-----SDDAEEDETLKKYKEDCLSTKTF----- 670
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 559 KSRMRPGLGYNENQIHKLDKVNESHAKRLQVPOECQVKQOASLVTHGKRKRVVHETR 618
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 671 -----GKRRTLSATSQL--SATFNKLPRSEMTLLCNEAIVLYMKALSLSKSQVTSNMW 723
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 619 NHLRLVGCVAACNTENAGVOESLSKLE-----LSHQLLDQRAK 659
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 724 YESQEKSCSLRV--NLVYLQMLREKFNCKLEKADFLRLKINDLRFKHA5EVAENGTLEE--K 780
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 660 GAOASPPPIAPPSPPKRLLLHMOELCGMKILASDL 697
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 781 GSSEEP-----VYLEKLLYDRALEISKMAHMEIKGENTL 814
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Search completed: May 14, 2002, 17:32:05
Job time: 1518 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 14, 2002, 17:32:13 ; Search time 142.98 seconds
(without alignments)
866,306 Million cell updates/sec

Title: US-09-582-397A-2
Perfect score: 3674
Sequence: 1 MOSTANYIMHTDLAGGAT.....LDDNRIIEIRLNVPAEPDV 716

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rv1rus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by charge to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1719.5	46.8	729	4	Q9UHD2
2	1711.5	46.6	729	11	Q9DC03
3	1710.5	46.6	729	11	Q9WUN2
4	1169	31.8	711	5	Q9V3Y8
5	434.5	11.8	756	6	Q95KV0
6	395	10.5	740	6	Q95KVL
7	386.5	10.3	731	5	Q9U7F5
8	379.5	10.3	731	5	Q9GTV6
9	377.5	10.3	741	5	Q9VEZ5
10	377.5	10.3	731	5	Q9U698
11	373.5	10.2	751	5	Q9NM11
12	347	9.4	732	5	Q61565
13	307	8.4	1036	4	Q75119
14	303	8.2	1037	11	Q9WTP4
15	303	8.2	1037	11	Q9YX01
16	298.5	8.1	729	11	Q9JKE4

17	298	8.1	1090	5	Q9N9J2	Q9N9J2 leishmania
18	296	8.1	1311	4	Q9ULE2	Q9ULE2 homo sapien
19	296	8.1	1315	4	Q9NRP7	Q9NRP7 homo sapien
20	294	8.0	454	4	Q43293	Q43293 homo sapien
21	293	8.0	1097	10	Q9SK42	Q9SK42 arabidopsis
22	292.5	8.0	520	5	Q9VHE6	Q9VHE6 drosophila
23	292	7.9	1090	5	Q9GRT3	Q9GRT3 leishmania
24	290.5	7.9	729	4	Q60219	Q60219 homo sapien
25	286.5	7.8	688	4	Q9BYD8	Q9BYD8 homo sapien
26	286	7.8	1497	5	Q95YH6	Q95YH6 drosophila
27	286	7.8	1571	5	Q95YH7	Q95YH7 drosophila
28	286	7.8	1612	5	Q9VE37	Q9VE37 drosophila
29	285	7.8	744	11	Q9JKE5	Q9JKE5 mus musculu
30	284	7.7	608	4	Q9C098	Q9C098 homo sapien
31	283.5	7.7	689	4	Q96JG7	Q96JG7 homo sapien
32	283.5	7.7	752	4	Q96L34	Q96L34 homo sapien
33	282.5	7.7	795	4	Q9P0L2	Q9P0L2 homo sapien
34	281	7.6	480	10	Q43380	Q43380 avena sativ
35	280.5	7.6	316	4	Q9NUJ5	Q9NUJ5 homo sapien
36	279.5	7.6	478	5	Q62571	Q62571 suberites d
37	278	7.6	744	4	Q96RGI	Q96RGI homo sapien
38	277.5	7.6	504	11	Q9QY26	Q9QY26 mus musculu
39	275.5	7.5	370	4	Q9UTK4	Q9UTK4 homo sapien
40	275.5	7.5	370	11	Q9QYM4	Q9QYM4 mus musculu
41	275	7.5	835	5	Q9VUL4	Q9VUL4 drosophila
42	274.5	7.5	370	4	Q75892	Q75892 homo sapien
43	274.5	7.5	832	5	Q963E5	Q963E5 drosophila
44	274.5	7.5	938	5	Q9YBV8	Q9YBV8 drosophila
45	274.5	7.5	1058	5	Q963E5	Q963E5 drosophila

ALIGNMENTS

RESULT 1
ID Q9UHD2 PRELIMINARY: PRT: 729 AA.
AC Q9UHD2;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TANK BINDING KINASE TBK1 (NF-KB-ACTIVATING KINASE NAK).
GN TBK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN;
RX MEDLINE-20050564; PubMed-10581243;
RA Pomerantz J.L., Baltimore D.;
RT "NF-kB activation by a signaling complex containing TRAF2, TANK, and
RL TBK1, a novel IKK-related kinase.";
RL EMBO J. 18:6694-6704(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-20244479; PubMed-10783893;
RA Tojima Y., Fujimoto A., Delnase M., Chen Y., Hatakeyama S.,
RA Nakayama K., Kaneko Y., Nimura Y., Motoyama N., Ikeda K., Karin M.,
RA Nakayama M.;
RT "NAK is an IkappaB kinase-activating kinase.";
RL Nature 404:778-782(2000).
RL EMBL: AF191838; AAF05989.1; -
DR EMBL: AF174536; AAF69106.1; -
DR InterPro: IPR00719; Euk_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase
SQ SEQUENCE 729 AA; 83642 MW; B50E4FE1B502276D CRC64;

Query Match	Best Local Similarity	Matches 352; Conservative 121; Mismatches 216; Indels 41; Gaps
QY 1	46.6%; Score 1711.5; DB 11; Length 729;	
Db 1	48.2%; Pred. No. 2e-120;	
QY 1	1	1
Db 1	1	1
QY 61	61	61
Db 61	61	61
QY 121	121	121
Db 121	121	121
QY 181	181	181
Db 181	181	181
QY 241	241	241
Db 241	241	241
QY 301	301	301
Db 301	301	301
QY 361	361	361
Db 361	361	361
QY 421	421	421
Db 421	421	421
QY 486	486	486

Db 481 VY-----EKLKVV--NEAEELGEISDIHKKLLRLSSQGTIESLQDISRLSPGL 531
 QY 524 NRELVSQDVH-EDRSIOQIOCCLDKMFYKQFKSSMRPGLGYNEQIHLKDVNS 582
 Db 532 LADTMAHOGSTHPRDRNVEKLVQVLLNCTEITYQFKKDAERLAEANEQIHKFDQKLY 591
 QY 583 HLAKRLLQVFOECVQKQYQASLVTHGKRMRVYHETRNHLRLVGCVAACNTAEQVQESL 642
 Db 592 YHATKAMSHFSECEKRYEAFKDKSEEMRKMLHLKROL-----SLTNOCFDIEEEV 644
 QY 643 SKL-----LEELSHOLLQDRAKGAQSPPIAPYSPTRKDLMLHCEGCMKLASD 696
 Db 645 SKQDYTNELQETLPQKMLASGVVHMAPIY-SSNTLVEMTGMKKLEMEGVKE 703
 QY 697 LLDNNRIIER 706
 Db 704 LANNHILIER 713

RESULT 3
 Q9WUN2 PRELIMINARY; PRT: 729 AA.
 AC Q9WUN2:
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE 12K PROTEIN KINASE HOMOLOG.
 GN TBK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=SMISS-WEBSTER/NIH;
 RA Mianowski D., Marcy A.L.;
 RT *Mus musculus homolog to human T2K cDNA.*;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RX MEDLINE=20050564; PubMed=10581243;
 RA Pomerantz J.L., Baltimore D.;
 RT *NF-kB activation by a signaling complex containing TRAF2, TANK, and
 RL EMBU J. 18:6694-6704(1999).
 DR EMBU; APL45705; AAD34590.1;
 DR EMBU; APL91839; AAP05990.1;
 DR MGD; MGI:1929658; TBK1.
 DR InterPro; IPR000719; Euk_pkinase.
 DR Pfam; PFO0069; Pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; kinase; transferase
 SQ SEQUENCE 729 AA; 83424 MW; 978ADDE3061DACD1 CRC64;

Query Match 46.6%; Score 1710.5; DB 11; Length 729;
 Best Local Similarity 48.6%; Pred. 2,4e-120;
 Matches 352; Conservative 119; Mismatches 224; Indels 29; Gaps 7;

QY 1 MOSTANTYIMHTDGLGCGATASYKANKKSGELVAVKVFNTSYLRPREVQREFEVL 60
 Db 1 MOSTSNHMLSLDILGCGATANVFGRHKKTGLYAVKVFNNISFLRPVYQKREFEVL 60
 QY 61 KLNHONVYKFAVEETGSGKQVLMFYCGSSGLSLVLESPENAFGLPDEFEVLVLCVY 120
 Db 61 KLNHKNVYKFAVEETGTHHKVLMFYCPGSLVTVLEPPSNAYGLPESEFLVLRDVY 120
 QY 121 AGNHLRENGIVHRDIPKGNIMRLVGEESQIYKLPDFGARELDDKRVSYGTEEYL 180
 Db 121 GGNHHLRENGIVHRDIPKGNIMRVIGSDQSVYKLPDFGARELDDKRVSYLGTREYL 180

QY 181 HPMYERAVLRKPOQKATGVVWLMISIGVTLVHAATGSLPPIPEGCPRRNKEIMYRTTE 240
 Db 181 HPMYERAVLRKPOQKATGVVWLMISIGVTLVHAATGSLPPIPEGCPRRNKEIMYRTTE 240
 QY 241 KPAAGVAGORENPLEMSTYLPITCOLSIGSOVLPIIANITIEVQAKMGDQFPA 300
 Db 241 KPAAGVAGORENPLEMSTYLPITCOLSIGSOVLPIIANITIEVQAKMGDQFPA 300
 QY 301 ETSIDLORVNVVAFSLQAVLHHIYIHAHNTYAIQEAHVHKTQSVAPRHQEFEGHLCV 360
 Db 301 ETSIDLORVNVVAFSLQAVLHHIYIHAHNTYAIQEAHVHKTQSVAPRHQEFEGHLCV 360
 QY 361 LEPSVAOHIAHTTASPPLTLFTSTAI PKGLAFRDPALDPKFPVVDVQADYVTKAGVYG 420
 Db 361 LEPSVAOHIAHTTASPPLTLFTSTAI PKGLAFRDPALDPKFPVVDVQADYVTKAGVYG 420
 QY 421 AGYQALRLARALDDQELMFRGLHVMVEVLAQTCRRL-----EVARSTL 465
 Db 421 VVCYACRTASTLLYQELMRKGVRLVLELVQDYNEVYAKKTEVYITLDFCI RNLEKTVK 480
 QY 466 LYLSSIGTERFSVAGTPEIOELKAAELRSRLTAEVLSRCSQNTIETQESLS--SL 523
 Db 481 VY-----EKLKVV--NEAEELGEISDIHKKLLRLSSQGTIESLQDISRLSPGL 531
 QY 524 NRELVSQDVH-EDRSIOQIOCCLDKMFYKQFKSSMRPGLGYNEQIHLKDVNS 582
 Db 532 LADTMAHOGSTHPRDRNVEKLVQVLLNCTEITYQFKKDAERLAEANEQIHKFDQKLY 591
 QY 583 HLAKRLLQVFOECVQKQYQASLVTHGKRMRVYHETRNHLRLVGCVAACNTAEQVQESL 642
 Db 592 YHATKAMSHFSECEKRYEAFKDKSEEMRKMLHLKROL-----SLTNOCFDIEEEV 644
 QY 643 SKL-----LEELSHOLLQDRAKGAQSPPIAPYSPTRKDLMLHCEGCMKLASD 696
 Db 645 SKQDYTNELQETLPQKMLASGVVHMAPIY-SSNTLVEMTGMKKLEMEGVKE 703
 QY 697 LLDNNRIIER 706
 Db 704 LANNHILIER 713

RESULT 4
 Q9V3Y8 PRELIMINARY; PRT: 711 AA.
 AC Q9V3Y8:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE 1K2 PROTEIN,
 GN IK2 OR DIX2 OR CG2615.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Abmayyan A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benson P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacled J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Inohara N.;
 RT "DIR2, Ikk-1 like protein.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003667; AAF5911.1; -;
 DR EMBL: AF197914; AAF04851.1; -;
 DR Flybase: FBgn0028633; IK2.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00240; ubiquitin; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 2.
 DR KATP-binding; kinase; transferase.
 KW SEQUENCE 711 AA; 81091 MW; 406CB82661262B60 CRC64;

Query Match 31.8%; Score 1169; DB 5; Length 711;
 Best Local Similarity 38.5%; Pred. No. 1.6e-79;
 Matches 262; Conservative 129; Mismatches 225; Indels 64; Gaps 14;

OY 1 MOSTANTYHMTDLDLGGATASVYARKKSGELVAVKFNTSYLRPREVOYFEVLR 60
 DB 4 LKGSVYVWCTSVLKGKATGSGVGVKKTGESVAVKTFNYSIMRADYQMRFEALK 63
 OY 61 KLNHONIKYKLVAVETGSGRQKVLVMEYCGSSGLSVLESPENAFGLPEDEFLVLCV 120
 DB 64 KYNHENIKYKLVAVETGSGRQKVLVMEYCGSSGLSVLESPENAFGLPEDEFLVLCV 123
 OY 121 AGMNLHRENGIYHDKICGNIMRLVGEKGSITKLTDFGARELDDDEKFSVYCTEYL 180
 DB 124 AGMKHLRDKKLVHDKICGNIMRLVGEKGSITKLTDFGARELDDDEKFSVYCTEYL 183
 OY 181 HPDMTERAVLRKPOQKAGVTVLMSIGVTLVYHAATGSLPFIPEGPRNKEIMRTITE 240
 DB 184 HPDLERAVLRKSIQSRFTANVDLMSIGVTLVYHAATGSLPFIPEGPRNKEIMRTITE 242
 OY 241 KPAAGIAGQRENGPRLKSTLPTCOLSLGLOSOLVPLIANTILEVBOAKCWGDFDFA 300
 DB 243 KASGVISGTQISENGPRLKSTLPTCOLSLGLOSOLVPLIANTILEVBOAKCWGDFDFA 302
 OY 301 ETSDLORVYVFSLSQAVLHHIYIHAANTIAIQAENVHNOTSVARPHQEVLRG-HLC 359
 DB 303 EYTLILKRVIVFTNTSSVEVLEPDEQIDNFERIRIQTQTEVPLEKQILLENNEHL- 361
 OY 360 VLEPSVAQHIAHTASSPLTFS-----TAIPKGLARFDALDPK---FVPRKVLQAD 411
 DB 362 -----EKKVPRTIDQPIFLYSMDNDNVQLPQ-----QIDLKPRVPPPNVSVND 407

OY 412 YNTAKVLAGYQALRLARALLDQGLMREGLHVMVEVLAQTCRRTEVARTSLITYSS 471
 DB 408 ASLAKSACSVEHCKRRDITSDILKKVEHFTEMLVTTTLTKTESPNDLSTV 467
 OY 472 LG-TERFSSVA-----GPEIOLKAAAE-LRSRLRTLAELVSRSCQNTITEQESLSLR 525
 DB 468 IDYADVVMARVWKGDEIKTLLALENVASDPDGAADYISQMKHFIYDDE---LND 523
 OY 526 ELVSRQDVH-----EDRSIQIQCCIDKKNFTYKQFKSRMRBGLGYNEODIKIDKY 579
 DB 524 QWTS--MHGKKCPCKTRASQAKVLERLRDWMHLLDRATRTLTLYNDEQFHALEKI 580
 OY 580 NESHLAKRLQVFE-----ECVQYQASLVYNGKRMVYHETRNHLRYGCSVA 629
 DB 581 KVDHNGKRIKRLLDNNVPTAQAIECLADWYKLAQTVYIKTQILER-----DVR 630
 OY 630 ACNTPAQGVQESLSKLEEL 649
 DB 631 DCEKRLNGIRDELVHVKSEL 650

RESULT 5
 ID Q95KVO PRELIMINARY; PRT; 756 AA.
 AC Q95KVO;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE IKB KINASE-BETA.
 GN BIRKBEA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rotenberg S., Dobbelaere D.A.E., Heusaler V.T.;
 RT "Identification and characterisation of the bovine IKB kinases (IKBs)
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A414556; CAC93687.1; -;
 KW kinase.
 SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query Match 11.8%; Score 434.5; DB 6; Length 756;
 Best Local Similarity 22.6%; Pred. No. 4.4e-24;
 Matches 180; Conservative 122; Mismatches 305; Indels 189; Gaps 23;

OY 9 WHTDLDLGGATASVYARKKSGELVAVKFNTSYLRPREVOYFEVLRKLNQNTY 68
 DB 15 WEKMERLGTGFGVNVIMHNOETGBOIAIKCOQELSPRRERWCLQIOTMRLLNPNV 74
 OY 69 KLFVABE-----TGSSRQKVLVMEYCGSSGLSVLESPENAFGLPEDEFLVLCVAGM 124
 DB 75 AARDVPEGMOSLAPNDPLLAEMEYCGSGDLKYLNFENCGGAREALITLSDIASAIR 134
 OY 125 HLRNGIYHDKICGNIMRLVGEKGSITKLTDFGARELDDDEKFSVYCTEYLHPDM 184
 DB 135 YLHNRILHDLKRENVLVLDQOGBQ-RLIHKIIDLGAKELDQSLCTSPVGLQYLAPEL 193
 OY 185 YERAVLRKPOQKAGVTVLMSIGVTLVYHAATGSLPFIPEGPRNKEIMRTITE 238
 DB 194 LE-----QKTYVADWISFGTLAFECTSPFRPLPMDQVOMHRSVRKQSEMDIYV 245
 OY 239 TERKAGIAGQRENGPRLKSTLPTCOLSLGLOSOLVPLIANTILEVBOAK-----CM 293
 DB 246 SED-----LNGAVFSSSLPRLPNLNSVLNQRLEKMTQDLMLNHPRGRTDPRY 294
 OY 294 GFDOFPAETSDIILORVVVHFSLSQAVLHHIYIHAANTIAIQAENVHNOTSVARPHQEV 353

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Db 295 GNGCFKALDDTLNLKHLVLMNTGLTHTYPTVEDESLOSARINRODTIGLEDEDEL 354
Oy 354 FEGHLCVLEPVSASOAHIAHTTASSPLTLESTAI-----PGCLA--F 392
Db 355 QEAGLALLIPDKPAACLSGKLNBRITLMDLFLFEDNSRVYVESQVSPQPSVSCIL 414
Oy 393 RBPALDVPKFKVQLQADYNFAKGVLAGVQALRLARALLDGOELMRGLHWMEVLOA 452
Db 415 QEKKRLPPE-----OLKRWGQVWHSI-----QALKE 442
Oy 453 TGRRTLEVARTSLLYL-----SSSLGTERESSVAGTPEI----- 486
Db 443 DCSRLQGGQRAAMNMLRNNSCTSKMKNSMSOOLKAKLDFEKTSLQIDLEKREOTE 502
Oy 487 -----QELKAALBSR---LRTLAEVSRSQNTTEQES----- 519
Db 503 FGITSDKLLANREMOAVALCGRENEVKHLVERMALOTDVLDRSPMGKOGGTLDD 562
Oy 520 LSLNRELV-----KSRDQVHEDRS-----IQOICCLDKMFIYQFKSRMRPGLG 567
Db 563 LERQARELVRLREKPRDRTGDSOEMRLLLOAIQGEKKVRYITQLSKT-----V 617
Oy 568 YNEEQIHLKDKVNFSLAKRLLOVQECVQYQASLVTHGKRMVHETRNHLRVGCS 627
Db 618 CKQKALELPKV-----EEVY-----SLMSEDEKVVRLQEKROKELMNL 658
Oy 628 VAACNT---EAGCVQESLSKLEELSH--QLLODRAKGAQSPPIAYPSTRKDLLH 682
Db 659 KICGSVYRGVSGSPDSMN--ASRLSHPCQLMSQ-----PCYAPSLPEAAKESDLVAE 711
Oy 683 MOELCEGMKLLASDL 698
Db 712 AHRLCTQLENAADPM 727

RESULT 6
O95KV1 PRELIMINARY; PRT; 740 AA.
AC O95KV1;
DT 01-DEC-2001 (TREMUREL. 19, Created)
DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)
DE IKB KINASE-ALPHA.
GN BIKKALPHA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT "Identification and characterisation of the bovine Ikb kinases (IKKS)
RL alpha, beta and gamma."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBD databases.
DR EMBL: AJ14555; CAC93686.1; -
KW Kinase.
SQ SEQUENCE 740 AA; 84343 MW; 01903BE1F44D176 CRC64;

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Query Match 10.88; Score 395; DB 6; Length 740;
 Best Local Similarity 23.0%; Pred. No. 4,1e-21;
 Matches 168; Conservative 114; Mismatches 309; Indels 138; Gaps 26;

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Oy 9 MHTDGLGCGATASVYKARKKSGELVAVVFNTSTYLRPREVQVEEVEYLKRLKINONTY 68
Db 15 WEMERLGTGFGVAVLCYOHRELDKTAIKSRELSTKREKMCHEIQMKMLNANV 74
Oy 69 KLFVVEETG---SRQVLYVMEYSSGSLSVLESPENAFGLPEDEFVLVRCVAGMNH 125
Db 75 KACQVPELNLVNDVPLAMEYCSGDLRLKLNKPCNCGLESQILSLDLSIGSIRY 134
Oy 126 LRENGIYHRIKPGNIMRVGEESQIYKLTDFCAARELDDEKFSVYVTEEYLHPDM 185

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Db 135 LHENKLIHRDLKAPENIV-LQDVGKIMKRIIDLYAKVDQSLCTSPVGTQLAPLELF 193
Oy 186 ERAVLRRPOAKFAGVVDLWISGIVLYHAATGSLPI-----PFGRRNKKEINRIITEK 241
Db 194 E-----NKPYATAVDWISFETWFEICIAGYRFLHHLOFTVHEKIK-----KK 237
Oy 242 PAGAIAGORERENGPLEWSTLP---ITQLSLGLOSOLPILAN-----ILEVE 288
Db 238 DPKCIFACEEM-TGEVRFPSHLRPPNSLSCLVPERMENNLOLMWDDQGRGPPVDLLK 296
Oy 289 QAKCWGFDQFAETSDILQVVVHVSLSQAVLHHIYIHAHTIAIFQPAVHKOTSVA 348
Db 297 QPRC-----FVLMHILMLKIYHILMNTSAKIIISFLPPEDSLHLSQSRIERETGINTG 350
Oy 349 HOEVLPE-----GHLCVLEP-----SVASQNIHAHTTASSPLTLPSCAIPKGLA 391
Db 351 SQELISEMGISLDPKRPASOCVLDGVGCDSTWVYLFDKSKTYVEGPRASNSLSQVNTI 410
Oy 392 FRPDALDVPKF-VPKV-----DLQADYNFAKGVLAGVQALRLARALLDGOELMR 441
Db 411 VQDSKIOLPIQLKRYMAEAVHVSGLKEDYSRL-----FOGGAAMLSTL---LRYN 459
Oy 442 GLHWMEVLOATCRRLTAVARTSLYLSSSLGTERPS--VAGTEPIQELKAALBSRL 499
Db 460 TNLTKMNTLISASQOLK-AKLEFFHKSIOLEDERSEQMTYGISSEKMLKAMKEMEKA 518
Oy 500 RTLAEVSRSQNTTEQESLSLNRELVKSRDQVHEDRSIQOICCLDKMFIYQFK 559
Db 519 ITHAEV-----GVYGLIEDQIMSLHTEIMELQSPYGRQGDLMESLEDRALDYLKQLH 573
Oy 560 SRMRPG-LGYNEQD-----IHKLD-----KVFSLAKRLLOVQECVQY----- 600
Db 574 ---RPSDSYSDSTPEWKIIVHTVQSDRVLRKELFGLSKL-----CKQKIIDLPLK 624
Oy 601 -----QASLVTHGKRMVHETRNHLRVGCSVAAC---NTEAGCVQESLSK 644
Db 625 VEMALSIKKEADSTVMQGRKEIW---HLTKIACYSARSLSVGLSVLPOLPP 680
Oy 645 LLEELSHQL 653
Db 681 TSAEREHPL 689

RESULT 7
O9UTF5 PRELIMINARY; PRT; 731 AA.
AC O9UTF5;
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DE CACTUS KINASE IKK.
GN IRD5 OR CG4201.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Medzhilov R.M., Janeway C.J.;
RT "Cloning and characterization of the Drosophila cactus kinase."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBD databases.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF128403; AAF04348.1; -
DR FLYBase: FBgn0024222; Ird5.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 731 AA; 84157 MW; 15381A6AD1EB343 CRC64;

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QY 577 ---DKVNFSLAKR-----LLOVFOECVQYQASLVTHGKRRRVVHETRNHLRLVGC5V 628
 DB 633 KSIDHHNYLYFKTESIPVLLQOF----- 656
 QY 629 AACNTEAGVQSLSLKLELBSHQLLDRAKGAQASPPRIAPSPTRKDLLHMOELCE 688
 DB 657 --CDIKKEIFQINLOLM-----SASSTPPP-----KLELSAANDRLAI 693
 QY 689 GKMLASDLDNNRIT-----ERLNRV 710
 DB 694 SSGSPSSDPFDSLRTINALEAERINNI 721
 RESULT 9
 QYVEZ5 PRELIMINARY: PRT: 741 AA.
 AC 09VEZ5: 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE IKK PROTEIN.
 GN IRDS OR IKK OR CG4201.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RX STRAIN=BERKELEY;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kension J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Modary C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF003711; AAF55267.1; -
 DR FlyBase: FBgn0024222; trds.

DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 KW ATP-binding; Serine/threonine-protein kinase; transferase.
 SQ SEQUENCE 741 AA; 85146 MW; 546616C8F964974B CRC64;
 Query Match 10.3%; Score 377.5; DB 5; Length 741;
 Best Local Similarity 23.1%; Pred. No. 8.5e-20;
 Matches 187; Conservative 111; Mismatches 311; Indels 199; Gaps 28;
 QY 1 MOSTANYLMHTDLDGATASVYKARKKSGELVAVFNTTSYLRPREVQVREFEVLAR 60
 DB 35 MHSFGN--WERCRLNGEGGFGVLIHMRNRRTGRELATGHIKEMGAL-SADQVYKSEKWN 91
 QY 61 K-----LNHONIVKLFAYEETG-----GSRQVLYMEKCGSSGLSLVLESFEN 103
 DB 92 KELNMSRQFKNPHIVAGVIEDPDEPLEYLNQMFSAKLPVLYLEVCGNDGVRKRLQSPEN 151
 QY 104 AFGPEDEFLVYRCVAGMNLREN-GIVHRDIKPGNIMRLVGEQSIYKIDPFGAAR 162
 DB 152 ANGLETFEYRQILGALRKALNPLHSQCGICHRDLRPNIVIORGVGDKKIKYKIDFGLAR 211
 QY 163 ELDDDEKFPVSYGTEBYLHPMYERAVLRKPOKAFQVTVLMSIGVLYHAATGSLPFI 222
 DB 212 GTPDQTVQSVGVGRHYVAPREVENG-----YNSVDLMSFGVIAVELYTGELPFI 263
 QY 223 PGFGRRKKEIMYRTTEKPAIAGAQRE-NGLEMSYTPITPCOISLGLQSLV--- 278
 DB 264 PR---QTKNIIILN-IKRPACIAITTEDPDNTFPVNOFELPQTHLSRPAADFTKWL 319
 QY 279 --PILANILEVQAKCMGDFQFAETSDILQRVVHVESLSQAVLHHIYHIMNTAIFQ 336
 DB 320 ASPLNSNTERKQGLAANNPVYFADLDKILNNVLTIFAVNCCERLEFAVSKMTKMDLI 379
 QY 337 EAVNHQTSVAPRHOEYLEGHLCVLEPSVAOCHIAHTASSPLTLESPAIPKGLAFRPA 396
 DB 380 ALIVLDTGMDKELEYFL-----PSSHKKITTPKSTPLQLYVE-----EMSDTS 424
 QY 397 LDVPR-----FVKKVLDQDYNKAGVLDAGVQALRLAALLDQGLMRGL-H 444
 DB 425 KQSRKWTKRNPVYLVYFQVKKEDCYKIPRILSI-----LSKRFYANK--EKTKER 475
 QY 445 WYME--VLOATCRRTLEVARTSLY-----LSSIGTERFSSVAGTP 484
 DB 476 WLOKRVYLDMLVYLRQARTEMVLSGINKERLSLEDEMENSFTDSIDKQIITISPAVD 535
 QY 485 EIQELKAAELRSRLTTLA-----EVLRSQONITETQESLSL-----NRELKSRD 532
 DB 536 QLSLTKKQAKIPSRQLSSAQWEMKLNNTNFIIOSAKSINSFLEACLRKADWKTN 595
 QY 533 QVHEDRSIOIOCC-----DKMNPYQFKSKRRRPGIGYBEOIHL- 576
 DB 596 QLRKEVCEEDLDCAFRYKYLNGAIIISPSELNDAEFAFSRKL--YMGGARHLPL 652
 QY 577 ---DKVNFSLAKR-----LLOVFOECVQYQASLVTHGKRRRVVHETRNHLRLVGC5V 628
 DB 653 KSIDHHNYLYFKTESIPVLLQOF----- 676
 QY 629 AACNTEAGVQSLSLKLELBSHQLLDRAKGAQASPPRIAPSPTRKDLLHMOELCE 688
 DB 677 --CDIKKEIFQINLOLM-----SASSTPPP-----KLELSAANDRLAI 713
 QY 689 GKMLASDLDNNRIT-----ERLNRV 710
 DB 714 SSGSPSSDPFDSLRTINALEAERINNI 741
 RESULT 10
 QYVEZ5 PRELIMINARY: PRT: 751 AA.

AC 090698:
 DT 01-MAY-2000 (TREMBLER, 13, Created)
 DT 01-MAY-2000 (TREMBLER, 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)
 DE IKK-LIKE PROTEIN.
 OS IRD5 OR CG4201.
 GN Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Inohara N., Nunez G.;
 RT "DIK, a IKK-like protein of Drosophila."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF190636; AAF04130.1; -.
 DR FlyBase: FBgn0024222; Ird5.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR AMP-binding: Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 751 AA; 86344 MW; 0060CEFA4BCB30A CRC64;
 SQ

Query Match 10.3%; Score 377.5; DB 5; Length 751;
 Best Local Similarity 23.1%; Pred. No. 8,7e-20;
 Matches 187; Conservative 111; Mismatches 311; Indels 199; Gaps 28;

QY 1 MOSTANTYLMHTDILGOGATASVYKARKKSGELVAHVNTTSYLREVOVREFEVLR 60
 DB 35 MHSFGN-WERCRLNIGEGGFLVIMRNRTGRIATKHIEKML-SADQVVKLSRW 91
 QY 61 K-----LNHONIVKLVAEETG-----GSRQKLVMEYCGSSGLSTVLESPEN 103
 DB 92 KELNMSROFKNPPIVAGVDIEDPDLFLYNGMFSAKLPVIVLECGGDVRRKRLOSPEN 151
 QY 104 AFGLEDEFLVLRGVAVAGNHLREN-GIVHRDIPGIMRLVGEQGSYTKLDFGAR 162
 DB 152 ANGLTEFEVRQILGALKRKALHFLHSQCGICHRDLKPNIVYIGRGVDCKIKYKLTDFGAR 211
 QY 163 ELDDDEKFEVSYGTEELHDMYRAVLRKPOKAFGVTVDLMSIGVTLVHAAGSLPFI 222
 DB 212 GTPDQTWQSVGTRHYIYAEVENG-----YNSTVLMISFGVIAVELVGTGLPFI 263
 QY 223 PFGGPRNKEIMYRITTEKPAAGAGORRE-NGPLEMSTLPTITQOLSLGLOSLV---278
 DB 264 PH---QTLKNTIILNL-IKKRAKCAITIEDPEDNTRFVNOPELFTQTHLSRPMMAOFTKWL 319
 QY 279 --PLANILEVEQAKKCGDPOFAETSDILQRVVAVHFSLSQAVLHHIYVHAHNTAIFQ 336
 DB 320 ASPLNSNYKRGOLAGNNVPEVADVDKILNMNVLTIFAANNCEBLEYANASAMTKMDLI 379
 QY 337 EAVHAKQSVAPRHOEYLFEBHLGVLEPSVAQHIAHTTASPLTFLSTAIKGLAFRPA 396
 DB 380 ALIVLDGMDEKELYFL-----PTSHPKTITPKSTPLQLYE-----EWSDS 424
 QY 397 LDYPR-----FVPRVLDADYNTAKGVLAGYALRLARLALLOGLMFGGL-H 444
 DB 425 KDSKAKWKRSNPVPMALYFOVKKEDYKTIPEPLST-----LSKRFITANK---EFTKER 475
 QY 445 WYME--VLAOTCRRTLEAVATSLY-----LSSSLGTERFSSVAGTP 484
 DB 476 WLRKRVYLDMLYVLTQRARYEMVSGINERALSLEDMMENSFIDSIOKRIILISFAD 535
 QY 485 EIELEKAAALRSRLRLA-----EYLSRQSUNITEOESLSL-----NRELKSD 532
 DB 536 QVLSLKEADAKIPSRQLISSAQEKLNRYNFIQSASIRSFLEACUREAKDWKTIN 595
 QY 533 QVHEDRSIQIOCCCL-----DKMNFYKQKKSRMRPGLGYNQEIHKL- 576

DB 596 QLRKEVCEKDLFDCARFYKKYLNGALISPSSELNDAEEFAFSRFL---YDEGRHLP 652
 QY 577 ---DKNVEFLAR-----LQVFOECYOKTOASLVTHGKRRVYHETRNHLRLVGC 628
 DB 653 KSIDHMYLYFKTKESIPVLLQF----- 676
 QY 629 AAGNTEAGVQESLKLLEELSHQLQDRAKQAQASPPILAVPSPTRKDLLHMQELCE 688
 DB 677 --CDIKKEIFQINQIMLM-----SASSTIPP-----KLELSAANDRLAI 713
 QY 689 GKMLASDLDNNRII-----ERLNRV 710
 DB 714 SSGSPSSDPDSIRITINALEARINNI 741

RESULT 11

ID 09NUT1 PRELIMINARY; PRT; 731 AA.

AC 09NUT1:
 DT 01-OCT-2000 (TREMBLER, 15, Created)
 DT 01-OCT-2000 (TREMBLER, 15, Last sequence update)
 DT 01-OCT-2001 (TREMBLER, 18, Last annotation update)
 DE LPS-RESPONSIVE KINASE.
 GN IRD5 OR IKK OR CG4201.
 OS Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20102723; PubMed-10636911;
 RA Kim Y.S., Han S.J., Ryu J.H., Choi K.H., Hong Y.S., Chung Y.H.,
 RA Perrot S., Rabbaud A., Brey P.T., Lee W.J.,
 RT "Lipopolysaccharide-activated kinase, an Essential Component for the
 RT Induction of the Antimicrobial Peptide genes in Drosophila
 RT melanogaster Cells."
 RL J. Biol. Chem. 275:2071-2079(2000).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF140766; AAF27291.1; -.
 DR FlyBase: FBgn0024222; Ird5.
 DR InterPro: IPR000345; Cyclic_heme_bind.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR ATP-binding: Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 731 AA; 84257 MW; 6F9CD54F6727312 CRC64;
 SQ

Query Match 10.2%; Score 373.5; DB 5; Length 731;
 Best Local Similarity 23.3%; Pred. No. 1.7e-19;
 Matches 187; Conservative 110; Mismatches 316; Indels 191; Gaps 28;

QY 1 MOSTANTYLMHTDILGOGATASVYKARKKSGELVAHVNTTSYLREVOVREFEVLR 60
 DB 15 MHSFGN-WERCRLNIGEGGFLVIMRNRTGRIATKHIEKML-SADQVVKLSRW 71
 QY 61 K-----LNHONIVKLVAEETG-----GSRQKLVMEYCGSSGLSTVLESPEN 103
 DB 72 KELNMSROFKNPPIVAGVDIEDPDLFLYNGMFSAKLPVIVLECGGDVRRKRLOSPEN 131
 QY 104 AFGLEDEFLVLRGVAVAGNHLREN-GIVHRDIPGIMRLVGEQGSYTKLDFGAR 162
 DB 132 ANGLTEFEVRQILGALKRKALHFLHSQCGICHRDLKPNIVYIGRGVDGKFKYKLTDFGAR 191
 QY 163 ELDDDEKFEVSYGTEELHDMYRAVLRKPOKAFGVTVDLMSIGVTLVHAAGSLPFI 222
 DB 192 GTPDQTWQSVGTRHYIYAEVENG-----YNSTVLMISFGVIAVELVGTGLPFI 243

QY 223 PFGGRNKKRMYRITTEKAGALAGQRR-NGPLEMSTYLPITCOLSLGLOSQV--- 278
 Db 244 PH---QTLKNIILNL-IRKPAKCAITDEDEDEMTREYNOGELDQTHLSRPMAGQFTKWL 299
 QY 279 --PLIANILEVEQAKCWGFDOFPAETSDILQRVVHVFSLSQAVLHHIYTHANTIAIFQ 336
 Db 300 ASPLNSYKRRGOLANNVVVFADLDKILMMVLTIFAVNCCERLEYAVSAETKMDLI 359
 QY 337 EAVHKOTSVAPRHOEYLFEGHLCVLEPVSQAHIANTTASSPLTLF-----STALPKG 389
 Db 360 ALIVLDGMDEKELLYFVL-----PTSHPKTITPKSTPIQLVYEWMSYTSKDSRKW 410
 QY 390 LARFDPALDVPKFPYKQADADYNIAKGVAGYQALRLALDQGLMFRGL-HYVME 448
 Db 411 TKSNP--PVMYTFQYKKCCDKYIPKPIST-----LSRKFTANK---FKTKERWLQK 459
 QY 449 --VLOATCRRTLEVARTSLY-----LSSSLGTERFSSVAGTPEIOE 488
 Db 460 RYVLIDLIVLTKEQAREMYLVSGINERALSLEDEMENSFIDSIDKRIITISFAYDQTS 519
 QY 489 LKAAELRSRLTLA-----EVLRSQNTTETQESLSL-----NRELVSQDVHE 536
 Db 520 LLEAQAKIRSRQLISSAQWELNRNRYNFIQSAKISRSFLACLRKAKMVKTNQOLRK 579
 QY 537 DRSIQIOGCL-----DKNFTYKOFKSRMRPGLGNEQIHL-----D 577
 Db 580 EYCEKOLFPCARFYKYLKGALISPSLNNDAEEFAKSRFL--YNEGEARHLPKSID 636
 QY 578 KVNFSLAKR-----LLQVQEBQVQYQASLVTHGKRMRVHEHTRNHLVLCGSAACN 632
 Db 637 HHMYLFKTESIPVLLQGF-----CD 658
 QY 633 TEAQVQESLSKLEESHOLODRAKGAQSPPIAPYSPPRKDLLHMOELCEGMKL 692
 Db 659 IKKEITQINIQMLM-----SASTPPT-----KLIELSAMDRLAISGSS 697
 QY 693 LASDLDDNNRII-----ERLNRV 710
 Db 698 PSSDPEDSLRTINAIEAEKINNI 721
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 061565 PRELIMINARY; PRT: 732 AA.
 AC 061565; 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
 GN I-KAPPA-B KINASE.
 OS Crassostrea gigas (Pacific oyster).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
 OC Ostreoida; Ostreidae; Crassostrea.
 OX NCBI_TaxID=29159;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99332074; PubMed=10405163;
 RA Escoubas J.M., Briant L., Montagnani C., Hez S., Devaux C., Roch P.;
 RT "Oyster Ikr-like protein shares structural and functional properties
 with its mammalian homologues";
 RL FEBS Lett. 453:293-298(1999).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF051320; AAC05683.1; -;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; kinase; Serine/threonine protein kinase; transferase.
 SQ SEQUENCE 732 AA; 84215 MW; 871EB8DCA3E39AF CRC64;

Query Match

9.4%; Score 347; DB 5; Length 732;

Best Local Similarity 22.8%; Pred. No. 1.7e-17;
 Matches 173; Conservative 126; Mismatches 320; Indels 140; Gaps 33;
 QY 9 WHTDLDLGGCATATSVYKARKKSGELVAVKVFNTTSYL--RPREVGVREVELRKLNHON 66
 Db 12 WIEVKTLISGGGQVVLKHHESRDDITALKCRVQSENMOKHKEKWTLEVDILKRLDHN 71
 QY 67 IYKLFAYE---ETGSGROKVLVMEYCSGSLSVLESPPENAGLPDEFLVLRGVVAGM 123
 Db 72 VIAKQVPELVNHYGEMPLAMEYCSGGDLKRVLNKPCNGCIAGYDRLCLVROLASAV 131
 QY 124 NHLRENGIYHRDIKPCGNIMRLVGEESQSYKLTDFGANELDDEKFEVSVYTEEYLPD 183
 Db 132 EYLHKRRRIIHRDLKPNIV-LHPTEDQTYKKVLDLGAKELODSSKCTSFVGMOLAPE 190
 QY 184 MYEYRAVLRKPOOKAFGVTVDLMSIGVTLHNAATGSPLRPFQGP-RRNKEIKYRITTEP 242
 Db 191 LF-----ASQKYCTYDMSFGIVVECTIGFEPFLPHVPYTWMEVY-----QKS 237
 QY 243 AGAIAQARRNGPLEMSTYLPITCOLSLGLOSQVLPILANILEVE-QAKCWGFD--QF 298
 Db 238 QDDITGFY-NSDGEVYFSQKILPTHLCSMQAYFQWLSLMLRMDSQLRGGRDGRPHC 296
 QY 299 FAEISDILQRVVHVFSLSQAVLHHIYTHANTIAIFQAVHKOTSVAPRHOEYLFEGHL 358
 Db 297 FRYLDTMLNVKILHLIYPCNOLSLVPLEVNSLOELQEKIKETGVKVEDDILLASGA 356
 QY 359 CVLEPVSQAHIANTTASSP-----LTLPFS-----TAIPKGL-----APRDPALD 398
 Db 357 SP-DPMLG---AHQCTWAPGEEDWVFLFAKGENOGGSQLOKPLPTVAGIETPTIV 411
 QY 399 VPKFVPR-----VD---IQADYNTAKGVLAGYQALRLALDQGLMFR 440
 Db 412 LPQEQKKAWEAVYVPCNOQVDFRLQSORAAML.SMLRTNDFPAKRRKKVSCSEHLV 471
 QY 441 RGLHVMVEVLOATCRTELEVARTSLY--LSSSLGTERSSVAGPPEI-QELKAAELRS 497
 Db 472 SKDYEELQ---HDLF-----LYGIQSRDGGISAERKVAKKKVEEMKLYHSLE 521
 QY 498 RLRTAEVLSRCSQNTTETQESLSLNRRLVKSQDVHEDRSIQIOGCLDKNFTYKQF 557
 Db 522 NYQTLHQSLAQTLELQKS-----PFRKTKOHE--VLENLESTAKKCTELOYDM 571
 QY 558 KSRMRPGLGYNEE-QIHKLDVNFVSHLAKRLQ--VFQEBQVQYQASLVTH-GRMRVY 614
 Db 572 RQA---GKGREYVKDHR-----PMVKLVKCIPTRD--QSLQ-DLYTHLKGKICACK 617
 QY 615 HETRNHLRLVGSVYACNTEAGV-----QESLSKLEESHOLODRAKGAQA 663
 Db 618 HELFOLLP---SIQCRQEDIGTQRLLOAHKOROSEIWSLVQMAEGMARQDSRSSGHA 673
 QY 664 SPPPIAPYSPPRKDLLHMOELCEGMKLASDLDDNNR 702
 Db 674 S-----MLSMY---GGASIDSTIKMCDNR 695
 RESULT 13
 075119 PRELIMINARY; PRT: 1036 AA.
 AC 075119; 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
 GN KIA0623; PROTEIN.
 DR KIA0623.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro."
 RL D.N. Res. 5:169-176(1998).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB014523; BAA31598.1; -
 DR HSSP: P24941; 1CKP.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 1036 AA; 112779 MW; CF73145EF37E641C CRC64;

Query Match 8.4%; Score 307; DB 4; Length 1036;
 Best Local Similarity 26.5%; Pred. No. 3e-14;
 Matches 104; Conservative 49; Mismatches 156; Indels 84; Gaps 11;

QY 1 MOSTANYLMTHTDLDLGAGATASYKARNK-KSGELVAVKVENTTSTYLRPREVQVREFEVL 59
 DB 1 MEVVGDFEYCKRDLYGHGAFVFRGRHROKTDMEVAIKSNKKNSQILLGKEIKIL 60
 QY 60 RKLNHQNIYKLFVVEETGSGROKVLVMEYCGSSGLSLVSEPNAGFLPEDEFLVLRVY 119
 DB 61 KELQHENITVALYVOELPNS--VFLVMEYCGSDLDLYLQAGT--LSEDTIRFLHQI 115
 QY 120 VAGMNLHRENGIVHRIKPGNIMRLVGEESQSI-----YKLTDFGAARELDDEKFSVY 174
 DB 116 AAAMRIILHSGIILHRLDKPQNILSLYANRRKSSVSGIRIKIADGFAARYLHNTMAATLC 175
 QY 175 GTEBYLHPDMTERAVLKRPOQKAFGVTVDLMSIGVTLVYNAATGSLPTIPFGGPRNKEIM 234
 DB 176 GSPMYMAPEVY-----MSQHYDAKADLMSIGTVLYOCVKGKPF-----QANSPOD 221
 QY 235 YRTTTERPAGAIAGORENGRPLEMSVTLPTGQLSLGLOSLQVPLANTILEVBOAKCWG 294
 DB 222 LRMETEKRSILMPSTPRE-----TSPYLANLLGL-----LQNKQDRMD 261
 QY 295 FDOFEAETSDILQRYVVVFFSLSQAVLHNIYIHANTIAIFQEAHVHKQTSVAPRHQETLF 354
 DB 262 FEAFES-----HPF-----LEQVPVKKSCPVPVPMYSGSV 291
 QY 355 EGHLCVLEPSV-----SAQHIATTTASSP 378
 DB 292 GSSGSSSPSCRFASPSPSLPDMOHIOEENLSSP 324

RESULT 14
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 AC Q9WTP4;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE UNC-51-LIKE KINASE (ULK) 2.
 GN ULK2 OR ULK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20027371; PubMed=10557072;
 RA Yan J., Kuroyanagi H., Tomemori T., Okazaki N., Asato K., Matsuda Y.,
 RA Suzuki Y., Ohshima Y., Mitani S., Masuno Y., Shitasawa T.,
 RA Muramatsu M.;
 RT "Mouse ULK2, a novel member of the UNC-51-like protein kinases: unique

RT Features of functional domains."
 RL Oncogene 18:5850-5859(1999).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB019577; BAA77341.1; -
 DR HSSP: P24941; 1CKP.
 DR MGD: MGI:1352758; ULK2.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 1037 AA; 112863 MW; D28E11B0B87E9613 CRC64;

Query Match 8.2%; Score 303; DB 11; Length 1037;
 Best Local Similarity 26.5%; Pred. No. 5.9e-14;
 Matches 104; Conservative 49; Mismatches 156; Indels 84; Gaps 11;

QY 1 MOSTANYLMTHTDLDLGAGATASYKARNK-KSGELVAVKVENTTSTYLRPREVQVREFEVL 59
 DB 1 MEVVGDFEYCKRDLYGHGAFVFRGRHROKTDMEVAIKSNKKNSQILLGKEIKIL 60
 QY 60 RKLNHQNIYKLFVVEETGSGROKVLVMEYCGSSGLSLVSEPNAGFLPEDEFLVLRVY 119
 DB 61 KELQHENITVALYVOELPNS--VFLVMEYCGSDLDLYLQAGT--LSEDTIRFLHQI 115
 QY 120 VAGMNLHRENGIVHRIKPGNIMRLVGEESQSI-----YKLTDFGAARELDDEKFSVY 174
 DB 116 AAAMRIILHSGIILHRLDKPQNILSLYANRRKSSVSGIRIKIADGFAARYLHNTMAATLC 175
 QY 175 GTEBYLHPDMTERAVLKRPOQKAFGVTVDLMSIGVTLVYNAATGSLPTIPFGGPRNKEIM 234
 DB 176 GSPMYMAPEVY-----MSQHYDAKADLMSIGTVLYOCVKGKPF-----QANSPOD 221
 QY 235 YRTTTERPAGAIAGORENGRPLEMSVTLPTGQLSLGLOSLQVPLANTILEVBOAKCWG 294
 DB 222 LRMETEKRSILMPSTPRE-----TSPYLANLLGL-----LQNKQDRMD 261
 QY 295 FDOFEAETSDILQRYVVVFFSLSQAVLHNIYIHANTIAIFQEAHVHKQTSVAPRHQETLF 354
 DB 262 FEAFES-----HPF-----LEQVPVKKSCPVPVPMYSGSV 291
 QY 355 EGHLCVLEPSV-----SAQHIATTTASSP 378
 DB 292 GSSGSSSPSCRFASPSPSLPDMOHIOEENLSSP 324

RESULT 15
 Q9QY01 PRELIMINARY; PRT; 1037 AA.
 AC Q9QY01;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SERINE/THREONINE KINASE UNC51.2.
 GN ULK2 OR UNC51.2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=BRAIN;
 RX MEDLINE=20088285; PubMed=10624947;
 RA Tomoda T., Bhatt R.S., Kuroyanagi H., Shirasawa T., Hatten M.E.;
 RT "A mouse serine/threonine kinase homologous to C. elegans UNC51
 RT functions in parallel fiber formation of cerebellar granule neurons."
 RL Neuron 24:833-846(1999).

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OM nucleic - nucleic search, using sw model

Run on: May 14, 2002, 17:28:58 ; Search time 8970.87 Seconds
(without alignments)
6788.218 Million cell updates/sec

Title: US-09-582-397a-3
Perfect score: 1 gaattcgacacgaagaata.....tttaaaaaaaaaaaaaaa 2910
Sequence: 1 gaattcgacacgaagaata.....tttaaaaaaaaaaaaaaa 2910

Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1556.4	53.5	3221	6	AX027541
3	1556.4	53.5	3221	6	D63485
4	1506.2	51.8	2154	9	AB016590
5	1501.6	51.6	2151	9	AF241789
6	529.6	18.2	2750	10	AF191839
7	528.2	18.2	2201	10	AF145705
8	468	16.1	2827	9	AF191838
9	468	16.1	2994	6	AR016417
10	468	16.1	2994	6	AR055686
11	468	16.1	3013	6	AX056361
12	468	16.1	3372	6	AF175112
13	466	16.0	2190	9	AF174536
14	432.8	14.9	228505	2	AC105704
15	357.8	12.3	2136	3	AF197914
16	340.2	11.7	11958	3	AC000245
17	340.2	11.7	156806	3	AC093047
18	340.2	11.7	263704	3	AE003667
19	328.2	11.3	32993	2	AC017993
20	202.4	7.0	142799	3	AC004759
21	188.8	6.5	228505	2	AC105704
22	160	5.5	56920	2	AC109262
23	149.8	5.1	107689	9	AL354681
24	139.4	4.8	376	11	G00776
25	104.2	3.6	56920	2	AC109262
26	84.2	2.9	2096	9	AK057159
27	74.6	2.6	3490	4	BTAA414556
28	68.2	2.3	1176	9	BC006231
29	68.2	2.3	2268	6	AR067807
30	68.2	2.3	2268	6	AR084022
31	68.2	2.3	2268	6	AR153351
32	68.2	2.3	2268	6	AR153423
33	68.2	2.3	2268	6	AR153426
34	68.2	2.3	2268	6	AX318491
35	68.2	2.3	2268	6	AF029684
36	68.2	2.3	2271	6	AR162236
37	68.2	2.3	2271	6	BD009912
38	68.2	2.3	2931	6	AR156758
39	68.2	2.3	3018	6	AX024044
40	68.2	2.3	3024	6	AX024040
41	68.2	2.3	3058	9	AF080158
42	68.2	2.3	3966	6	AR099305
43	67.4	2.3	3234	3	AF051320
44	67.2	2.3	775	6	AR103250
45	67.2	2.3	775	6	AX000638

ALIGNMENTS

RESULT 1
LOCUS AB016589
DEFINITION Mus musculus IKK-i mRNA for inducible Ikappab kinase, complete cds.
ACCESSION AB016589
VERSION AB016589.1 GI:6012173
KEYWORDS IKK-i; Inducible Ikappab kinase.
SOURCE Mus musculus macrophage cell_line:RAW264.7 cDNA to mRNA, clone_ltb:lamba Zap.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Shimada,T., Kawai,T., Takeda,K., Matsumoto,M., Inoue,J., Tatsumi,Y., Kanamaru,A. and Akira,S.
TITLE IKK-i, a novel lipopolysaccharide-inducible kinase that is related to Ikappab kinases
JOURNAL Int. Immunol. 11 (8), 1357-1362 (1999)
MEDLINE 99352266
REFERENCE 2 (bases 1 to 2893)
AUTHORS Akira,S. and Shimada,T.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-1998) Shizuo Akira, Hyogo College of Medicine,

Department of Biochemistry; Mukogawa-cho 1-1, Nishinomiya, Hyogo
663-8501, Japan (E-mail: akira@hyo-med.ac.jp, Tel: 81-798-45-6357,
Fax: 81-798-46-3164)

FEATURES

Location/Qualifiers
1. 2893

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/db_xref="taxon:10090"
/cell_line="RAN264.7"
/cell_type="macrophage"
/clone_11b="lambda ZAP"

gene

CDS

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AKLDDKRFVSYGTVEYLHMDYERANLKRPOKAFQVTVDDLSIGVTLHAATGS
LPTIPGGRNKEIMYRITTEKPAISGTOKEGPLEMSYSLPTICRLSMGLQNO
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PLGSLINEQIHKLDKYNFSLHKLRLQVDEKVCQYQVSLVTHGHRNQVRAQNLH
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2893

polya_site

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BASE COUNT 689 a 781 c 798 g 625 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
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DB 61 GCATACGATGACCTGCTAGGCGAGGGGCCACTGCCAGTGTGACAAAGCCCGAAACAA 120
QY 121 gaaatccggggaggtgtgtctgttaaaaggtcttcaactcagccagctatcgggacctcc 180
DB 121 GAAATCCGGGGAGGTGTGCTTAAGGCTTCAACTCAGCCAGCATGAGGGGACTCC 180
QY 181 tgaagttcaggtgagaggtttgagtcctcggagaggtcgaatcaccagaacatcgtgaa 240
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DB 241 GCTATTTCGCAAGTGAAGGAGGAGGAGCGGACAGAAAGGTGCTAATGAGAGTACTG 300
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RESULT 2
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DEFINITION Sequence 1 from Patent W00039308.
ACCESSION AX027541
VERSION AX027541.1 GI:10188451
KEYWORDS
SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 3221)
AUTHORS Sakai, Y., Hashimoto, Y. and Takemoto, Y.
TITLE IKK3 kinase
JOURNAL Patent: WO 0039308-A-1 06-JUL-2000;
SAKAI YUTAKA (JP); GLAXO WELLCOME KABUSHIKI KAISHA (JP); HASHIMOTO
YASUHIRO (JP); TAKEMOTO YOSHITIRO (JP)
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ORIGIN

Query Match 53.5%; Score 1556.4; DB 6; Length 3221;
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QY	1460	accgaa-----ggttaagaagtggctc--ggagatgctgtcgtccaggaagaaagg	1513
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QY	1514	gcacagagctaaagaaccagcgtctgagactctctcaagaatcctgtctctaaatgtctccac	1573
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QY	1688	aagatgacctcatctacaacaagctcaagaatccagatgtaaggccaaggtcctcagctac	1747
Db	1683	TGCATTCACAGAGATTACTATTCAGTTCAAAAAGAAACAAAGACAGAAACGACATAGCTTAT	1742
QY	1748	aatgagggacagatccacacaagctgtgataagtaattcaatctcatctagccaaaggagctg	1807
Db	1743	AATGAAGAAACAGATCCACAAATTTGATTAAGCAAAAATTTGATTAACCATGTGCCACAAAAGCA	1802
QY	1808	ctgcagctgtctcagaggagtggtgtgcagacgfatataagtgctcgtgtgtcacacacgycg	1867
Db	1803	ATGAGCACACTTCTCAGAAAGATGTGTGAAGAAAGTATCAACGCTTTAAAGTAAATGCTGGAA	1862
QY	1868	aagcgatgagagcaaggtgcagaggcccgaaacacactg	1906
Db	1863	GAGTGGATGACAAAGATGCTTCACTTTAAGGAAGCAGCTG	1901

RESULT	8
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LOCUS	2827 bp mRNA linear PRI 08-DEC-1999
DEFINITION	Homo sapiens TANK binding kinase TBK1 (TBK1) mRNA, complete cds.
ACCESSION	AF191838
VERSION	AF191838.1 GI:6224867
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 2827)
Pomerantz, J.L. and Baltimore, D.
NF-kappaB activation by a signaling complex containing TRAF2, TANK
and TRB1, a novel IKK-related kinase
EMBO J. 18 (23), 6694-6704 (1999)

JOURNAL
20050564

MEDLINE
2 (bases 1 to 2827)

REFERENCE
Pomerantz, J.L. and Baltimore, D.
Direct Submission
Submitted (04-Oct-1999) Biology, California Institute of
Technology, 1200 East California Boulevard, MC 147-75, Pasadena, CA
91125, USA

FEATURES
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/product="TANK binding kinase TRB1"
/protein_id="AA05989.1"
/db_xref="GI:6224868"
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BASE COUNT
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ORIGIN

Query Match 16.1% Score 468; DB 9; Length 2827;
Best Local Similarity 59.3%; Pred. No. 2.1e-102;
Matches 817; Conservative 0; Mismatches 555; Indels 6; Gaps 1;

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121 CTGCAATGCTCTTCGTGGAGACATAGAAACTGGTGAATTTTTCATCAAGATAT 180
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181 TTAATAAATCAATAGCTTCTGCTCAGTGGATGTTCAATAGAGAAATTAAGTGTGA 240
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333 accctgagaacacgctcgggcttctgaagagaggttccctggtgtcgtcgtgtgtg 392
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393 tggctggcctgagacacccgaggagatgcatcttcacatggagacataaccctgga 452

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453 acatcatcgctcgtgtgtgagagagagggcagagcattcattaaagctgtcgtcgtg 512
481 ATATCATCGCTTATATAGGGAAGATGGACAGTCTGTGTACAACTCAACAGATTTTGGTG 540
513 ctgcgcgaagctgagacatgatagaagttgttctcgtcgtcgtcgtcgtcgtcgtcgtc 572
541 CAGCTAGAGAAATTAAGAAATGATGAGAGTGTGTTCTCTATGACAGCAAGAAATATT 600
573 tgcacccagacatgataagcgtgagcgtgcgcgaacccagcaaaagcattgtgtg 632
601 TGCACCTGATATGATATAGAGAGAGTGTGTAAGAAAGATCATCAGAAATATATGAG 660
633 tgacgtgatactcgtgagatctggtgtgacccgtgacacgacgacagcagctgtgc 692
661 CAACAGTGTATGTTTGGAGCATTTGGGTAACATTTTACATGACAGCTACTGATCAGTGC 720
693 ccttaccctcctcgtgtgtgagcccgagcaacaagaatcattacagatccacacag 752
721 CATTTAGACCTTTGAGAGCCCTCCTAGGAATAAAGAGTATATAAATAATTACAG 780
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1113 tcttgacaaagcctcctcagccagcagacatcgccacacagctgcagcagcctctaa 1172
1141 TCTTAGAACCTGGAAGCTGAGCACAACATTTCCCTAAACTACTGAGAAACCTTAT 1200
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LOCUS
DEFINITION Sequence 1 from patent US 5776717.
ACCESSION AR016417
VERSION AR016417.1 GI:3972694

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2994)
TITLE I. kappa.B kinases
JOURNAL Patent: US 5776717-A 1 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..2994
BASE COUNT 1018 a 489 c 611 g 876 t
ORIGIN

Query Match 16.1%; Score 468; DB 6; Length 2994;
Best Local Similarity 59.3%; Pred. No. 2.1e-102;
Matches 817; Conservative 0; Mismatches 555; Indels 6; Gaps 1;

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153 tcaactcagccagctatcgcgagacctctgaagltcaagltgaaggaglttgaagtcctgc 212
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LOCUS AR055686 2994 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5837514.
ACCESSION AR055686
VERSION AR055686.1 GI:5981263
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2994)
TITLE I. kappa.B kinases
JOURNAL Patent: US 5837514-A 1 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..2994
BASE COUNT 1018 a 489 c 611 g 876 t
ORIGIN

Query Match 16.1%; Score 468; DB 6; Length 2994;
Best Local Similarity 59.3%; Pred. No. 2.1e-102;
Matches 817; Conservative 0; Mismatches 555; Indels 6; Gaps 1;

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RESULT 11
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LOCUS Sequence 5 from Patent WO0073469.
DEFINITION AX056361
ACCESSION AX056361
VERSION AX056361.1 GI:12229068
KEYWORDS
SOURCE
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 3013)
AUTHORS Ploeman, G.D., Martinez, R., Whyte, D. and Sudersanam, S.
TITLE Protein kinases
JOURNAL Patent: WO 0073469-A 5 07-DEC-2000;
Sugen, Inc. (US)
FEATURES
location/Qualifiers
source 1..3013
/organism="Homo sapiens"
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BASE COUNT 1017 a 496 c 619 g 881 t
ORIGIN

Query Match 16.18; Score 468; DB 6; Length 3013;
Best Local Similarity 59.34; Pred. No. 2.1e-102;
Matches 817; Conservative 0; Mismatches 555; Indels 6; Gaps 1;

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Qy 93 ctgcagctgctacagagcccgaaacaaagaatccgggagctgtgtcgtgaagct 152
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Qy 153 tcaactcagcagctacgagcagcctcctgagctgagctgagcagcagcagcagcagc 212
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Qy 213 ggaagcagctgaatcagcagcagcagcagcagcagcagcagcagcagcagc 272
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Qy 453 acatcatgcgcctggctgggaggaagggagagacatcctataagctgctcagctcggg 512
Db 511 ATATATCGCTGTATAGGGAGATGAGACAGTCTGTGTACAAATCTACAGATTTTGGTG 570
Qy 513 ctgcgcgaagctggaagcatgagaaagctgttctcgtcctatgtaacagaagaatacc 572

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QY 933 cggagaccagtgacattctctgacggaacgctccacacgctcttccctaccacgagccg 992
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 QY 993 ttctgacatgctacacacgccccacacacgattgcatcttcttgaggctglat 1052
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RESULT 13

LOCUS AF174536 2190 bp mRNA linear PRI 10-MAY-2000
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 ACCESSION AF174536
 VERSION AF174536.1 GI:7767392
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 SOURCE human.
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2190)
 AUTHORS Tojima,Y., Fujimoto,A., Delhase,Y., Chen,Y., Hatakeyama,S.,
 Nakayama,K., Kaneko,Y., Nimura,Y., Motoyama,N., Ikeda,K., Karin,M.
 and Nakanishi,M.
 TITLE NAK is an IkappaB kinase-activating kinase
 JOURNAL Nature 404 (6779), 778-782 (2000)
 MEDLINE 20244479
 PUBMED 10783893

REFERENCE 2 (bases 1 to 2190)
 AUTHORS Tojima,Y., Fujimoto,A., Hatakeyama,S., Nakayama,K., Kaneko,Y.,
 Nimura,Y., Motoyama,N., Ikeda,K., Karin,M. and Nakanishi,M.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-1999) Biochemistry, Nagoya City University
 Medical School, Kawasumi 1, Mizuho-ku, Mizuho-cho, Nagoya, Aichi
 467-8601, Japan
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Query Match 12.3%; Score 357.8; DB 3; Length 2136;
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 Job time: 19521 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	468	16.1	3013	22	AAF44626
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11	357.8	12.3	2187	23	ABL04897	Drosophila melanog
12	340.2	11.7	4518	23	ABL04896	Drosophila melanog
13	295.4	10.2	511	22	AAZ27175	CDNA encoding nove
14	264.2	9.1	3641	21	AAZ58582	Mouse protein kina
15	207.8	7.1	3511	23	ABL16432	Drosophila melanog
16	167.8	5.8	949	22	AAH95884	Human protein enco
17	165.4	5.7	538	22	AAZ27160	CDNA encoding nove
18	138.4	4.8	2371	21	AAZ58583	Mouse protein kina
19	92.6	3.2	198	21	AAZ41461	Human secreted exp
20	89.4	3.1	339	20	AAZ41125	Human secreted pro
21	85.2	2.9	302	20	AAZ40308	Human secreted pro
22	82.2	2.3	2268	20	AAZ31590	Human secreted pro
23	68.2	2.3	2268	20	AAZ98271	Human secreted pro
24	68.2	2.3	2268	20	AAZ98271	Human secreted pro
25	68.2	2.3	2268	20	AAZ98271	Human secreted pro
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ALIGNMENTS

RESULT 1	AAA52449	standard; CDNA; 2910 BP.
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DT	25-SEP-2000	(first entry)
XX		
DE	Murine I-kappa-B kinase (IKK-1) CDNA.	
XX		
KW	I-kappa-B kinase; IKK-1; murine; serine/threonine kinase; NF-kappa-B;	
KW	nuclear factor kappa-B; inflammation; immune disorder; TRAF molecule;	
KW	I-TRAF related disorder; antiinflammatory; immunostimulatory; ss.	
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PD	04-MAY-2000.	
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PE	26-OCT-1999;	99WO-JP05916.
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PR	26-OCT-1998;	98JP-0304085.
XX		
PA	(NISC-) JAPAN SCI & TECHNOLOGY CORP.	
XX		
PI	Akira S, Shimada T;	

XX WPI: 2000-350748/30.
 DR P-PSDB: AAB01980.
 XX
 XX Novel I-kappa-B kinase, IKK-1, capable of activating transcription
 PT factor NF-kappa-B to inhibit expression of gene relating to immune
 PT response, useful in drug compositions to treat inflammation and improve
 PT immune response mechanism
 PS
 PS Claim 5: Page 44-46; 52pp; Japanese.

XX This sequence represents cDNA encoding murine I-kappa-B kinase (IKK-1).
 CC IKK-1 is a serine/threonine kinase which can activate the transcription
 CC factor NF-kappa-B (nuclear factor kappa-B). The invention relates
 CC to the human and murine IKK-1 proteins (AAB01979, AAB01980), variants
 CC thereof, and to nucleic acids encoding human and murine IKK-1 (AAB52448,
 CC AAB52449). IKK-1 proteins are useful in drug compositions to treat
 CC inflammation and improve the immune response mechanism. They may also be
 CC used in preventing and treating diseases associated with the I-TRAF or
 CC TRAF molecule.

XX Sequence 2910 BP; 706 A; 781 C; 798 G; 625 T; 0 other:

Query Match 100.0%; Score 2910; DB 21; Length 2910;
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 Db 961 ggtatccagctcttccctacccagcagcagcagcagcagcagcagcagcagcagcagcag 1020
 QY 1021 caacagatgtccatcttctgtgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1080
 Db 1021 caacagatgtccatcttctgtgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1080
 QY 1081 ccagagtaacctcttctgagagtgacacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
 Db 1081 ccagagtaacctcttctgagagtgacacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
 QY 1141 catcgccacacagctgacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1200
 Db 1141 catcgccacacagctgacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1200
 QY 1201 taagtggtgtgcttctcaagagccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
 Db 1201 taagtggtgtgcttctcaagagccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
 QY 1261 cctacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1320
 Db 1261 cctacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1320
 QY 1321 gctgtgctggt 1380
 Db 1321 gctgtgctggt 1380
 QY 1381 ggaagtgcttcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1440
 Db 1381 ggaagtgcttcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1440
 QY 1441 cctcgagcagcagcctggtgacgtgagaggttcaagcagtgagtcgagagtgagtcgagtc 1500
 Db 1441 cctcgagcagcagcctggtgacgtgagaggttcaagcagtgagtcgagagtgagtcgagtc 1500
 QY 1501 ggaaggaagagagagcagagcagcagcagcagcagcagcagcagcagcagcagcagcag 1560
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Db 1741 cagctacaatgagagagacagatccacaaagctgtaagtaatttcagtcacatagccaa 1800
 Qy 1801 gaagcgcgcgcaagtgcttccaggaagagtgctgcaagagatcaagtgctgctgctac 1860
 Db 1801 gaagcgcgcgcaagtgcttccaggaagagtgctgcaagagatcaagtgctgctgctac 1860
 Qy 1861 acacggcaagcagatgagcagtgcaagagggccgaacacatcatalcatalcagccaa 1920
 Db 1861 acacggcaagcagatgagcagtgcaagagggccgaacacatcatalcatalcagccaa 1920
 Qy 1921 ctctgctgcaagcagtgcaagagggccgaacacatcatalcatalcagccaa 1980
 Db 1921 ctctgctgcaagcagtgcaagagggccgaacacatcatalcatalcagccaa 1980
 Qy 1981 tgatcagctcctctgcaagagagctccgaacagggagagtgctcagcgaacatc 2040
 Db 1981 tgatcagctcctctgcaagagagctccgaacagggagagtgctcagcgaacatc 2040
 Qy 2041 ggcctccatcccgccgctgacaggaagcctgctcctcagatgcaagcgttgtaa 2100
 Db 2041 ggcctccatcccgccgctgacaggaagcctgctcctcagatgcaagcgttgtaa 2100
 Qy 2101 tgatagaagctatgagccttgatctcgaagcaacacagcctatcgaagcgttaca 2160
 Db 2101 tgatagaagctatgagccttgatctcgaagcaacacagcctatcgaagcgttaca 2160
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 Db 2161 taagatccatccgcaagcagatgctgagctccctgaggggttacaagcagcagaagc 2220
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 Db 2221 aatagaacaatcatalatgacccctcagcctcagcagcaaatcagggagagcttctgt 2280
 Qy 2281 tcaatcctcagcagcagcctcctctctgagcagtgccatgagcagcaaatcagcagcagc 2340
 Db 2281 tcaatcctcagcagcagcctcctctctgagcagtgccatgagcagcaaatcagcagcagc 2340
 Qy 2341 ctctgagctgctcctctgaggaagcagcagcagcagcagcagcagcagcagcagcagc 2400
 Db 2341 ctctgagctgctcctctgaggaagcagcagcagcagcagcagcagcagcagcagcagc 2400
 Qy 2401 ctacagaagagacacatgagcagcagcagcagcagcagcagcagcagcagcagcagc 2460
 Db 2401 ctacagaagagacacatgagcagcagcagcagcagcagcagcagcagcagcagcagc 2460
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 Db 2521 ttcccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2580
 Qy 2581 aatgctatcctcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 2640
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 Qy 2641 ggcac 2700
 Db 2641 ggcac 2700
 Qy 2701 gctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2760
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Qy 2881 ggccttctgtcttaaaaaaaaaaaaaa 2910
 Db 2881 ggccttctgtcttaaaaaaaaaaaaaa 2910
 RESULT 2
 AA295275
 ID AA295275 standard; cDNA; 3385 BP.
 XX
 AC AA295275;
 XX
 DT 26-MAY-2000 (first entry)
 DE
 XX
 DE Murine I kappa B kinase-related kinase 1 encoding cDNA spQ ID NO:1.
 KW Mouse; murine; I kappa B kinase-related kinase; IKR-1; IKR-2;
 KW protein kinase; immunomodulatory; antiinflammatory; antimicrobial;
 KW cytosolic; autoimmune; inflammatory; infection; neoplastic disease; ss.
 XX
 OS Mus sp.
 XX
 PH key Location/Qualifiers
 FT CDS 370..2523
 FT /*tag= a
 FT /product= "IKR-1"
 FT /note= "I kappa B kinase-related kinase 1"
 XX
 PN WO200008179-A1.
 XX
 PD 17-FEB-2000.
 XX
 PF 04-AUG-1999; 99WO-US17578.
 XX
 PR 04-AUG-1998; 98US-0095269.
 PR 11-SEP-1998; 98US-0099973.
 PR 05-FEB-1999; 99US-0118783.
 XX
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 PI Bird TA, Virca GD;
 XX
 DR WPI: 2000-195583/17.
 DR P-PSDB: AAY80279.
 XX
 PT Novel kappa B-kinase related kinases IKR-1 and IKR-2 used as molecular
 PT weight markers and in peptide fragmentation studies -
 XX
 PS Claim 1: Fig 1: 85pp: English.
 XX
 CC The present sequence encodes murine I kappa B-kinase related kinase 1
 CC (IKR-1). IKR proteins have immunomodulatory, antiinflammatory,
 CC antimicrobial and cytosolic activities. IKR polynucleotides can be
 CC used to express the proteins, and as probes to identify nucleic acids
 CC encoding proteins having kinase activity. IKR-1 and IKR-2 proteins and
 CC fragmented polypeptides are used for purifying proteins, e.g. as quality
 CC binding partner proteins; to measure protein activity, e.g. as quality
 CC assurance agents to monitor shelf life and stability of binding partner
 CC proteins. They may also be used as research agents, e.g. in assays to
 CC determine protein kinase activity, to identify novel molecules involved
 CC in signal transduction pathways, and to identify therapeutic compounds,
 CC to identify substances which interfere with the rate of substrate
 CC phosphorylation (such compounds would be useful for the treatment of
 CC autoimmune, inflammatory, infectious or neoplastic diseases), as
 CC molecular weight and isoelectric focusing markers, as controls for
 CC peptide fragmentation, identification of unknown proteins, e.g. by
 CC comparison with proteins in databases and for preparation of antibodies.
 CC The antibodies can be used in assays to detect the presence of the
 CC protein, and to purify the protein by immunofluorescence chromatography. The
 CC antibodies can also be used to block binding of the IKR polypeptides to
 CC their binding partners.
 CC
 CC Sequence 3385 BP; 821 A; 922 C; 925 G; 717 T; 0 other:

QY 2113 attggccttgcattccaggacacacacgacatcatcgaacggttaccatagattccatc 2172
 Db 2448 atgggccttgcattccaggacacacacgacatcatcgaacggttaccatagattccatc 2507
 QY 2173 ggcacacagatgtctgagctccctgggggttcacaaagagcattcgaagcaatataaacatt 2232
 Db 2508 ggcacacagatgtctgagctccctgggggttcacaaagagcattcgaagcaatataaacatt 2567
 QY 2233 catattgtaccctaccatcctgtgagaccacaaatcgaaggcaagtctgttccatcacta 2292
 Db 2568 catattgtaccctaccatcctgtgagaccacaaatcgaaggcaagtctgttccatcacta 2627
 QY 2293 ggcctaccctccttggccattggccattggccacaaataaattacttacttaccgtcc 2352
 Db 2628 ggcctaccctccttggccattggccattggccacaaataaattacttacttaccgtcc 2687
 QY 2353 tcttgggaagcagcagtaagaaaggaactcctggccatcccgagcagatatacagaagaga 2412
 Db 2688 tcttgggaagcagcagtaagaaaggaactcctggccatcccgagcagatatacagaagaga 2747
 QY 2413 ccatggcggtaccacacagccttaccagaacacaaagactgttctcctaccagcctcgt 2472
 Db 2748 ccatggcggtaccacacagccttaccagaacacaaagactgttctcctaccagcctcgt 2807
 QY 2473 gaagtcgtgcttggaagaaaggaagcctcaccctcaccgcttgaactccacagagaca 2532
 Db 2808 gaagtcgtgcttggaagaaaggaagcctcaccctcaccgcttgaactccacagagaca 2867
 QY 2533 gcaagacatcctcgtgcttccctcctcctcaccaggggtgctgatacagaattacttct 2592
 Db 2868 gcaagacatcctcgtgcttccctcctcctcaccaggggtgctgatacagaattacttct 2927
 QY 2593 tgggtttctcgtgcttccctcctcctcctcctcctcctcctcctcctcctcctcctcct 2652
 Db 2928 tgggtttctcgtgcttccctcctcctcctcctcctcctcctcctcctcctcctcctcct 2986
 QY 2653 acggccctcctcgtgcttgcctagatgcacacatcatttgaagaagtggtgtgagagct 2712
 Db 2987 acggccctcctcgtgcttgcctagatgcacacatcatttgaagaagtggtgtgagagct 3046
 QY 2713 aactcgtgctgcttgaagaattcctcctgaacttctcctcgaaggaagcctgtgttctaa 2772
 Db 3047 aactcgtgctgcttgaagaattcctcctgaacttctcctcgaaggaagcctgtgttctaa 3106
 QY 2773 aaacacatgctgcttgaagaattcctcctgaacttctcctcgaaggaagcctgtgttctaa 2832
 Db 3107 aaacacatgctgcttgaagaattcctcctgaacttctcctcgaaggaagcctgtgttctaa 3166
 QY 2833 cctaaagagagcagcagcctgcacacatcagacatggaataaataacatcgccttcttct 2892
 Db 3167 cctaaagagagcagcagcctgcacacatcagacatggaataaataacatcgccttcttct 3226
 QY 2893 taataaataaataaataaataaataaataaataaataaataaataaataaataaataaataa 2910
 Db 3227 taataaataaataaataaataaataaataaataaataaataaataaataaataaataaataa 3244
 RESULT 3
 AAA47001
 ID AAA47001 standard; DNA; 3221 BP.
 AC AAA47001;
 XX
 XX
 XX 03-OCT-2000 (first entry)
 DE
 DE DNA encoding a human IKK3 kinase.
 XX
 XX Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT CDS 327..2477
 FT /*tag= a
 FT /product= "IKK3 kinase"
 XX
 XX MO200039308-A1.
 XX
 PD 06-JUL-2000.
 XX
 XX 24-DEC-1999; 99WO-JP07286.
 XX
 XX 24-DEC-1998; 98GB-0028704.
 XX
 PA (GLAXO) GLAXO WELLCOME KK.
 XX
 PI Takemoto Y, Sakai Y, Hashimoto Y;
 DR WPI: 2000-475700/41.
 DR P-PSDB: MAY93676.
 PT
 PT New IKK3 kinase protein and nucleotides encoding it, useful for
 PT screening for IKK3 protein modulators for treating inflammation, e.g.
 PT arthritis, atopic dermatitis or systemic lupus erythematosus
 XX
 PS Claim 5; Fig 4: 102pp; English.
 CC
 CC The present sequence encodes a human IKK3 kinase protein. The protein
 CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
 CC useful for screening for agents with anti-inflammatory activity
 CC compounds which exhibit IKK3 kinase modulating activity may be used
 CC in formulating a treatment or prophylaxis of a disorder responsive to
 CC the modulation of IKK3 kinase activity in a mammal. The proteins,
 CC their variants or fragments, derivatives, analogues or cells expressing
 CC them can also be used as immunogens to produce antibodies against IKK3
 CC protein, which may further be used to locate the protein in tissues
 CC expressing that protein.
 XX
 SO Sequence 3221 BP; 710 A; 941 C; 949 G; 621 T; 0 other:
 Query Match 53.5%; Score 1556.4; DB 21; Length 3221;
 Best Local Similarity 80.7%; Pred. No. 0;
 Matches 1908; Conservative 0; Mismatches 436; Indels 20; Gaps 7;
 QY 12 gagaagataagccaaagccagagatgcagagatcaccataacttctgtgacatgagtg 71
 Db 304 gaccagccagctcagagcagagatgcagagatcaccataacttctgtgacatgagtg 363
 QY 72 aactcgtgagcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 131
 Db 364 aactcgtgagcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 423
 QY 132 agtggtgctgttaagagctcctcaccatcagcagcagcagcagcagcagcagcagcagcag 191
 Db 424 agtggtgctgttaagagctcctcaccatcagcagcagcagcagcagcagcagcagcagcag 483
 QY 192 tgaaggagcttgaagtcctcctcgaagcgtgaatcaccagaacatcgtgaagctatctcag 251
 Db 484 tgaaggagcttgaagtcctcctcgaagcgtgaatcaccagaacatcgtgaagctatctcag 543
 QY 252 tgaaggaaacggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 311
 Db 544 tgaaggaaacggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 603
 QY 312 gctcgtgagcgtgctggaagacccctggaacacagcgtgagggcttctggaagagaggttc 371
 Db 604 gctcgtgagcgtgctggaagacccctggaacacagcgtgagggcttctggaagagaggttc 663
 QY 372 tagtggtcgtcgtcgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 431
 Db 664 tagtggtcgtcgtcgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 723
 QY 432 atcgggacatcaaaccttgggaacatcagcgcctgtgtggcagagagagagagagcattc 491

Db 724 atcgagacatcaagccgggagacatcatgctgcctcgttaaggaggagggagagcatc 783
 Qy 492 ataagctgtgacttcggggctgcccgaagctgagacgatgatgagaagtcttctctg 551
 Db 784 acaagctgacagacttcggggctgcccgaagctgagacgatgatgagaagtcttctctg 843
 Qy 552 tctatgtacagagaaatacctgacccctgacatgtatgacgctgacgctgacgacac 611
 Db 844 tctatgtacagagaaatacctgacccctgacatgtatgacgctgacgctgacgacac 903
 Qy 612 cccgagaaaagacattggtgtgactgtgactgtgactgtgactgtgactgtgactgtgac 671
 Db 904 cccgagaaaagacattggtgtgactgtgactgtgactgtgactgtgactgtgactgtgac 963
 Qy 672 acgagacacagagacgtgacgttcacccctcctcgtgagcccgcccgacgacaaaaga 731
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 Qy 732 tcatgtacagaaatcaacagagaaagccagccgggacatttcaggagactcaagaagcag 791
 Db 1024 tcatgtacagaaatcaacagagaaagccagccgggacatttcaggagactcaagaagcag 1083
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 Db 1084 agaacgggcccctgagagctacacccctcccatcaccctgtacagctgtcctgagc 1143
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 Db 1144 tgcagaaacagagctgtgacccatcctcgtgacacatcctgagagctgagagagataagct 1203
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 Db 1204 gggagcttgatcagcttctcgtgagagacagtgacatctcgtcagcgagacgtacacag 1263
 Qy 972 tctttccctcccccagggccgtttgtacatctgtctacatccagccacacacagcttg 1031
 Db 1264 tctttccctcccccagggccgtttgtacatctgtctacatccagccacacacagcttg 1333
 Qy 1032 ccatcttcttgagagctgtatatagtacagacaaagctgaccccccacacacagagatc 1091
 Db 1334 ccatcttcttgagagagctgtatatagtacagacaaagctgaccccccacacacagagatc 1383
 Qy 1092 tcttcgagagctacacccctgtgtctccttgagacacacacacacacacacacacacac 1131
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 Qy 1212 ccttcagagac 1271
 Db 1498 ccttcagagac 1557
 Qy 1272 attacagac 1331
 Db 1558 attacagac 1617
 Qy 1332 tcttcgtgagagac 1391
 Db 1618 tcttcgtgagagac 1677
 Qy 1392 aggaacacgtgcagac 1451
 Db 1678 aggaacacgtgcagac 1737
 Qy 1452 gctcgtgagac 1511
 Db 1738 gctcgtgagac 1797
 Qy 1512 aggcacacagac 1571
 Db 1798 aggcacacagac 1857

Qy 1572 acaatgtcacagaac 1631
 Db 1858 acaatgtcacagaac 1917
 Qy 1632 gggacacagatcactgagatcaac 1691
 Db 1918 gggacacagatcactgagatcaac 1974
 Qy 1692 tgcactcatcactcaac 1751
 Db 1975 tgcactcatcactcaac 2034
 Qy 1752 aggaacacagatcactgagatcaac 1811
 Db 2035 aggaacacagatcactgagatcaac 2094
 Qy 1812 aggtgttcacagagagctgt 1871
 Db 2095 aggtgttcacagagagctgt 2154
 Qy 1872 ggaatgagacagctgag 1931
 Db 2155 ggaatgagacagctgag 2214
 Qy 1932 cctgtac 1989
 Db 2215 cctgtac 2274
 Qy 1990 ccttcgtgacagagcttcac 2045
 Db 2275 ccttcgtgacagagcttcac 2334
 Qy 2046 ccttcgtgacagagcttcac 2105
 Db 2335 ccttcgtgacagagcttcac 2394
 Qy 2106 tgaagctatgtgac 2165
 Db 2395 tgaagctatgtgac 2454
 Qy 2166 ttcac 2225
 Db 2455 ttcac 2513
 Qy 2226 aaac 2283
 Db 2514 aaac 2572
 Qy 2284 atctac 2342
 Db 2573 atctac 2632
 Qy 2343 ttgactgtcctcttggaagacac 2366
 Db 2633 ttgactgtcctcttggaagacac 2656

RESULT 4
 AAAS2448
 ID AAAS2448 standard; cDNA; 2154 BP.
 AC AAAS2448;
 DT 25-SEP-2000 (first entry)
 DE Human I-kappa-B kinase (IKK-i) cDNA.
 DE I-kappa-B kinase; IKK-i; human; serine/threonine kinase; NF-kappa-B;
 DE nuclear factor kappa-B; inflammation; immune disorder; TRAF molecule;
 DE I-TRAF related disorder; antiinflammatory; immunostimulatory; ss.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH 3..2153
 FT /tag= a
 FT /product= "Human I-kappa-B kinase"
 XX WO200024908-A1.
 XX
 XX 04-MAY-2000.
 XX
 XX 26-OCT-1999; 99WO-JP05916.
 XX
 XX 26-OCT-1998; 98JP-0304085.
 XX
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 XX Akira S. Shimada T;
 XX
 XX WPI; 2000-350748/30.
 XX P-PSDB; AAB01979.
 XX
 XX Novel I-kappa-B kinase, IKK-1, capable of activating transcription
 XX factor NF-kappa-B to inhibit expression of gene relating to immune
 XX response, useful in drug compositions to treat inflammation and improve
 XX immune response mechanism
 XX
 XX Claim 5; Page 41-42; 52pp; Japanese.
 XX
 XX This sequence represents cDNA encoding human I-kappa-B kinase (IKK-1).
 XX IKK-1 is a serine/threonine kinase which can activate the transcription
 XX factor NF-kappa-B (nuclear factor kappa-B). The invention relates
 XX to the human and murine IKK-1 proteins (AAB01979, AAB01980), variants
 XX thereof, and to nucleic acids encoding human and murine IKK-1 (AA52446,
 XX AA52449). IKK-1 proteins are useful in drug compositions to treat
 XX inflammation and improve the immune response mechanism. They may also be
 XX used in preventing and treating diseases associated with the I-TRAF or
 XX TRAF molecule.
 XX
 XX Sequence 2154 BP; 482 A; 612 C; 668 G; 392 T; 0 other;

Query Match 51.8%; Score 1506.2; DB 21; Length 2154;
 Best Local Similarity 82.1%; Pred. No. 0;
 Matches 1775; Conservative 0; Mismatches 373; Indels 15; Gaps 3;

QY 33 agatgagagtaactaactactgtgtgcatatgatgacctgtcagcgagggcca 92
 DB 1 agatgagagtaactaactactgtgtgcatatgatgacctgtcagcgagggcca 60
 QY 93 ctgcagatgtgtacaagcgacgaacaagaatcgggaggtgtgtctgttaaggtct 152
 DB 61 ctgcagatgtgtacaagcgacgaacaagaatcgggaggtgtgtctgttaaggtct 120
 QY 153 tcaactcagcagactatctgagacccctcgtgaggttcaggttgagggaggtttgaggtcttcg 212
 DB 121 tcaactcagcagactatctgagacccctcgtgaggttcaggttgagggaggtttgaggtcttcg 180
 QY 213 ggaagctgaatcaccagaaacatcgttgaagctatctcagctgaggaacgggagcgacc 272
 DB 181 ggaagctgaatcaccagaaacatcgttgaagctatctcagctgaggaacgggagcgacc 240
 QY 273 ggcagaaggtgtcaatcattgaggtactgtctcaggtgaggaacgttcagcggtgtggaag 332
 DB 241 ggcagaaggtgtcaatcattgaggtactgtctcaggtgaggaacgttcagcggtgtggaag 300
 QY 333 accctgaagaacagcttcgggacttcggaagagaggttcaggttcaggttcggttcgtgtg 392
 DB 301 gccctgaagaacagcttcgggacttcggaagagaggttcaggttcaggttcggttcgtgtg 360
 QY 393 tggctgcagtaaccacccgcgaggaatgcatgttccatcgggacatcaaacctgggga 452
 DB 361 tggctgcagtaaccacccgcgaggaatgcatgttccatcgggacatcaaacctgggga 420

QY 453 acatcatgcccctggtggtgagaggggagagagatcatatgaactgtctgactcgagg 512
 DB 421 acatcatgcccctggtggtgagaggggagagagatcatatgaactgtctgactcgagg 480
 QY 513 ctgcccgaagctgtgacagatgataaggttctgtctgtctatgtatcagaagaatacc 572
 DB 481 ctgcccgaagctgtgacagatgataaggttctgtctgtctatgtatcagaagaatacc 540
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 QY 633 tgactgtgactctgagatgtggtgtgacccctgtacacgacgacgacgacgtcgc 692
 DB 601 tgactgtgactctgagatgtggtgtgacccctgtacacgacgacgacgacgtcgc 660
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 DB 1141 cctctgtcagcatgtccagcgaacacacacacacacacacacacacacacacacacacac 1194
 QY 1233 atgtccaaaggt 1292
 DB 1195 atgtccaaaggt 1254
 QY 1293 tctgtgagcgtgtcacaagcggt 1352
 DB 1255 tctgtgagcgtgtcacaagcggt 1314
 QY 1353 tgaatcctcggggtgtcaatgt 1412
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 DB 1435 gcaagtgtgaggt 1494
 QY 1533 ggtctgacagatctctcagagatctctgtctaaatgttcccaaatgttccagaaacccaaa 1592

XX 07-MAR-1997; 9705-0812533.
 PR (TULSA-) TULARIN INC.
 PA
 XX
 PI Cao Z;
 DR WPI: 1999-023452/02.
 DR P-PSDB: AAW79273.
 XX
 PT Recombinant or isolated nucleic acid encoding TRAF2-associated
 PT kinase - which regulates inhibitors of NF-kappaB transcription
 PT factors, useful as immunogen; for isolation of other transcriptional
 PT regulators; in drug screening; and in gene therapy
 PS
 PS Claim 4: Columns 9-16; 11pp; English.
 CC This cDNA encodes a TRAF2 (TRAF2-associated kinase) protein belonging to
 CC the family of IkappaB kinases. Cells containing a recombinant TRAF2 nucleic
 CC acid are used to produce the TRAF2 protein which is useful as immunogen,
 CC for isolation of other transcriptional regulators and in drug screening.
 CC The TRAF2 nucleic acid and corresponding antisense sequences, are useful
 CC in gene therapy to modulate TRAF2 expression, and its fragments are used as
 CC probes and primers in diagnostic assays (hybridisation or amplification),
 CC for identification of related sequences and to detect wild-type or mutant
 CC alleles. The TRAF2 nucleic acid can also be used to create transgenic
 CC animals for studying the efficacy of candidate drugs. TRAF2 binding agents
 CC are useful in diagnosis, therapy and drug development, e.g. they can
 CC activate, inhibit or alter TRAF2-dependent processes and activity of NF-
 CC kappaB transcription factor.
 XX
 SO Sequence 2994 BP; 1018 A; 489 C; 611 G; 876 T; 0 other;

Query Match 16.1%; Score 468; DB 20; Length 2994;
 Best Local Similarity 59.3%; Pred. No. 1.1e-119;
 Matches 817; Conservative 0; Mismatches 555; Indels 6; Gaps 1;

QY 33 agatgcagagtaaccactaactcctggtgcatatgatacctgtagggcaggggcca 92
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 QY 93 ctgcgcagctgtgtaacagagccggaagaagaatccgggaggtgtgtgtgtgtaaggtct 152
 DB 131 ctgcgcagctgtgtaacagagccggaagaagaatccgggaggtgtgtgtgtgtaaggtct 190
 QY 153 tcaactcagccagctatcgcgcagcctcctgaggttcaggtggaaggaggttggagctcctg 212
 DB 191 ttaataacataagctcctcctcctgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 250
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 DB 251 aaaaatacctacatacaaaaataatgttcaaaatatttgcatactggaaggaggaacaacaaa 310
 QY 273 ggcagaaggtgtaacatcagtagtactgtccaggtgggagcctgctgagcgtgtgtgaag 332
 DB 311 gacataaagtaactatgataagatttgcacatgtggaggttatacactgtttagaag 370
 QY 333 accctgagaacagctcgcgccttctgaaagaggaagttcctagtggtgcgcgtgtgtg 392
 DB 371 aaccttctaattgctatgatacagcaatcgaattccttaattgttggcagatgtgtg 430
 QY 393 tggctggatgaacacacgtcgcgggaagatgtgcatgtccatcgggaggaacaaacctgtgga 452
 DB 431 tgggtgtgaatcatctcactcagaagatgtgatacgcgtgatacagccagga 490
 QY 453 acatactgacctgtgtgtggcgggaggggagagacatcataagctgtgtgtcctcgagg 512
 DB 491 atatactgctgttataagggaagagacagctgtgtgaacaaacacagatttgggtg 550
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 DB 551 cagctagagaattagaagatgtgtgagcagttgtttctgtcaggtacagggagataacc 610

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 DB 791 gaaagcctctgt 850
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 DB 911 tctctgcaaacatcctgtgagcagatcaggaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 970
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 DB 1031 cagctcatagattatatacagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1090
 QY 1053 atgagcagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1112
 DB 1091 aaaaac 1150
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 QY 1353 tgaatcctcgggggt 1410
 DB 1385 taatgcgaagggagatacagatgt 1442

RESULT 8
 AAF44626
 ID AAF44626 standard; cDNA: 3013 BP.
 XX
 XX AAF44626;
 AC
 XX
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Novel protein kinase cDNA, SEQ ID NO: 5.
 XX
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; caridant; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;

Db 1111 ataacaacacaaatttcttcaatacagaactatctacgaagggcagccttag 1170
 Qy 1113 tcccttgagcgaagcctcgaagccagacacalcgcgcacacagctgcgcagccctctaa 1172
 Db 1171 tcttagaacctcggaaggtgtgcacacattccctaaacactacgaggaacacctatat 1230
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 Db 1285 cccctcccaaaagatcatccacgttatattagacggggatgcgtacgctggctaaaggcaa 1344
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 Qy 1353 tgatgcttcgggggttcatatgtgtcctggaagggtgccttcagacagctgcagcagac 1410
 Db 1405 taatgcgaaaagggtacagatgcgtgattgaatgaataagatgataatgaatgaac 1462

RESULT 11

ABL04897

ID ABL04897 standard; cDNA; 2187 BP.

AC ABL04897;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 9173.

KW Drosophila; developmental biology; cell signalling; insecticide;

KM pharmaceutical; gene; ss.

OS Drosophila melanogaster.

PN WO2001/71042-A2.

PD 27-SEP-2001.

XX 23-MAR-2001; 2001MO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EM;

DR WPI: 2001-656860/75.

XX P-P-SDB; ABB60794.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX

PS Claim 1; SEQ ID NO 9173; 21bp + Sequence Listing; English.
 XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB5737-ABB72072).
 CC

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcr_sequences.
 CC

SQ Sequence 2187 BP; 613 A; 510 C; 582 G; 482 T; 0 other;

Query Match

Best Local Similarity 12.3%; Score 357.8; DB 23; Length 2187;

Matches 624; Conservative 0; Mismatches 422; Indels 3; Gaps 1;

Qy 36 tgcagagtaacactaactactctgtgcatctatgcatgacccgctcagggcagggccactg 95
 Db 62 tgcgcggtctccgagagtaatgtgtgtgcacacacagcgtcccggaagggagccacg 121
 Qy 96 ccagtggtgtaacaggcccggaacacagaatccggggaggtgtgtgtgtgtgtgtgtgt 155
 Db 122 gttccgtgtcccgagggtgcataacagatccacgcgcgatactcgtggtgtgtgtgtgt 181
 Qy 156 actcagcacaactatcgcgcagccctcgaaggttaagtgaggaaggttgaagtcctcgga 215
 Db 182 atccctaacatcacatgacacgcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 241
 Qy 216 ggtcgtatccacaggaacatcgtgaagctatccgaagtgcagtgaggaacgggagcgagc 275
 Db 242 aggttcaacacaggaatataatagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 301
 Qy 276 agaatgtgtcaatcagagtaactgtctcagtggtgtgtgtgtgtgtgtgtgtgtgtgt 335
 Db 302 gtaaggtgactgt 361
 Qy 336 ctgagacacgttccgggttccgaagaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 395
 Db 362 ctgagaaactgt 421
 Qy 396 ctgagatgaacacacgt 455
 Db 422 ccggaatgaagcaacttgcgt 481
 Qy 456 tcatggtcgt 515
 Db 482 taatgaagttcatctcgt 541
 Qy 516 cccgcaagctggaacgtatgaagaattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 575
 Db 542 ctgagaaactgt 601
 Qy 576 accctgacatgtatgaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 635
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 Qy 636 ctgtgtatctctggaatgt 695
 Db 662 atgtgtatgt 721
 Qy 696 tcatcccttcgt 755
 Db 722 ttgacctttgt 778
 Qy 756 agccagcgggggacatttcaaggaactcagaagcaagaatgtgtgtgtgtgtgtgtgt 815
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 Db 899 tagctgtactctcgt 958
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 Qy 996 tgcattgttaccatccgcgcacacagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1055

KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW reproductive system; gastrointestinal; liver disorder; AIDS; ss;
KW acquired immune deficiency syndrome.
OS Homo sapiens.
XX WO200154733-A1.
XX 02-AUG-2001.
PD 17-JAN-2001; 2001WO-US01312.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0196123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 23-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0228509.
PR 05-SEP-2000; 2000US-0228513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231411.
PR 08-SEP-2000; 2000US-0231414.
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PR 08-SEP-2000; 2000US-0231414.
PR 12-SEP-2000; 2000US-0233081.
PR 12-SEP-2000; 2000US-0233081.
PR 14-SEP-2000; 2000US-0233297.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233063.

PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2002, 17:31:08 ; Search time 147.27 Seconds
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4853.626 Million cell updates/sec

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Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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2: /cgn2_6/prodata/2/ina/5b_COMB.seq:*
3: /cgn2_6/prodata/2/ina/6a_COMB.seq:*
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5: /cgn2_6/prodata/2/ina/PCtUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	16.1	2994	1	US-08-971-937-1 Sequence 1, Appl
2	468	16.1	2994	2	US-08-812-533-1 Sequence 1, Appl
3	68.2	2.3	2268	2	US-08-890-853-1 Sequence 1, Appl
4	68.2	2.3	2268	2	US-09-099-125A-1 Sequence 1, Appl
5	68.2	2.3	2268	2	US-09-099-124A-1 Sequence 1, Appl
6	68.2	2.3	2268	2	US-09-197-008-1 Sequence 1, Appl
7	68.2	2.3	2268	4	US-09-032-476-1 Sequence 1, Appl
8	68.2	2.3	2268	4	US-08-890-854-1 Sequence 1, Appl
9	68.2	2.3	2268	4	US-09-023-324-1 Sequence 1, Appl
10	68.2	2.3	2271	4	US-08-910-820-8 Sequence 1, Appl
11	68.2	2.3	2931	4	US-09-168-629-14 Sequence 8, Appl
12	68.2	2.3	3966	3	US-09-215-131-1 Sequence 1, Appl
13	68.2	2.3	3966	3	US-09-222-734-1 Sequence 1, Appl
14	67.2	2.3	775	3	US-09-124-476-1 Sequence 1, Appl
15	67.2	2.3	775	4	US-09-577-796A-1 Sequence 1, Appl
16	62.4	2.1	1468	3	US-09-215-131-2 Sequence 2, Appl
17	62.4	2.1	1468	4	US-09-222-734-5 Sequence 2, Appl
18	58.2	2.0	2146	4	US-09-032-476-5 Sequence 5, Appl
19	58.2	2.0	2146	4	US-08-890-854-5 Sequence 5, Appl
20	58.2	2.0	2146	4	US-09-023-324-5 Sequence 5, Appl
21	58.2	2.0	2238	2	US-08-890-853-3 Sequence 3, Appl
22	58.2	2.0	2238	2	US-09-099-125A-3 Sequence 3, Appl
23	58.2	2.0	2238	2	US-09-099-124A-3 Sequence 3, Appl
24	58.2	2.0	2238	4	US-09-032-476-3 Sequence 3, Appl
25	58.2	2.0	2238	4	US-08-890-854-3 Sequence 3, Appl
26	58.2	2.0	2238	4	US-09-023-324-3 Sequence 3, Appl
27	58.2	2.0	2251	4	US-08-910-820-7 Sequence 7, Appl

28	58.2	2.0	2273	2	US-09-197-360-1 Sequence 1, Appl
29	58.2	2.0	2273	4	US-09-168-629-1 Sequence 1, Appl
30	58.2	2.0	2273	4	US-08-810-131A-1 Sequence 1, Appl
31	57.2	2.0	2025	3	US-09-160-483-2 Sequence 2, Appl
32	54.8	1.9	5228	4	US-09-428-711A-15 Sequence 15, Appl
33	51.4	1.8	1302	1	US-08-913-050A-2 Sequence 2, Appl
34	51.2	1.8	2132	2	US-09-159-385-3 Sequence 3, Appl
35	51.2	1.8	2132	4	US-09-186-277-3 Sequence 3, Appl
36	50.8	1.7	3561	1	US-08-097-997A-12 Sequence 12, Appl
37	50.8	1.7	3561	3	US-08-665-574C-12 Sequence 12, Appl
38	50.8	1.7	3561	4	US-08-946-994-12 Sequence 12, Appl
39	48.4	1.7	1466	2	US-08-749-902-2 Sequence 2, Appl
40	46.2	1.6	7218	1	US-08-232-463-14 Sequence 14, Appl
41	45.2	1.6	7218	1	US-08-232-463-14 Sequence 14, Appl
42	43.6	1.5	2673	4	US-09-428-711A-1 Sequence 1, Appl
43	43.6	1.5	3995	4	US-09-428-711A-13 Sequence 13, Appl
44	43.4	1.5	1429	2	US-09-159-385-4 Sequence 4, Appl
45	43.4	1.5	1429	4	US-09-186-277-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-971-937-1
Sequence 1, Application US/08971937
Patent No. 5776717
GENERAL INFORMATION:
APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: TRAP2-Associated Kinase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,937
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/812,533
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 73..2259
US-08-971-937-1

Query Match 16.1% Score 468; DB 1; Length 2994;
Best Local Similarity 59.3%; Pred. No. 1.2e+118;
Matches 817; Conservative 0; Mismatches 555; Indels 6; Gaps 1;

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Qy 33 agatgcagagtlaccactactactctgtgcatctatgacccctgctaggcaggggcca 92
Db 71 AGATGCAGAGCAGCTTCTTAATCATCTGTGCTTTTACTGCTTAATTTTAAAGCCAAAGAGCTA 130
Qy 93 ctgcagctgtgtacaaagcccgaaacaagaatccgggggggtgtgtcgttgaagctc 152
Db 131 CTGCAGAAATGCTTTCGTGGAAGACATTAAGAACTGCTGATTTATTTGCTATCAAGATAT 190
Qy 153 tcaactcagcagctatccgacccctcgaaggtcaggtgagggaggtttgaggtcctgc 212
Db 191 TTATTAACATTAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250
Qy 213 ggaagcgtgaatccagagaatctgtagagctatccgaggtgaggaacggggagcc 272
Db 251 AAAACATCAATCAACAAATTAATTTCTCAATTAATTTGCTAATTAAGAGAGAGACACAA 310
Qy 273 ggcagaaggtgtactatcatgagagctgctccagtgaggacccctgtcagcgtcgtgaag 332
Db 311 GACATTAAGATCTTATATGGAATTTTGTCCATGTGGAGTTTATACACTGTTTAAAG 370
Qy 333 accctgagaacagcttcgggcttcctgaagaaggtccctcaggtgtcgtcgtgtgtg 392
Db 371 AACCTTCAATGCTTATGAGACTACCAATCTGAAATCTTAATGTTTGGAGATGTGG 430
Qy 393 tggcgtgcatgaaccacccctgggagagatgcatgtccatccgagacatacactgtgga 452
Db 431 TGGGTGGAATATCATCATCTACGAGAGATGCTATAGTGCACCCGATATCAAGCAGAGAA 490
Qy 453 acatcatgcgcctgtgtggaaggaagggcagagacatctataagctgtcgtcgtcgtg 512
Db 491 ATATCATGCTGTATAGGGGGAATGAGCATGCTGTGTACAACTCAAGATTTTGGTG 550
Qy 513 ctgcccgaagctggaagatgataagatgtttctgtctatgtagaaggaataacc 572
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Qy 633 tgaactgtgactctgtgagatgttggtgtgacccctgtacacgcagcagcagcagctgc 692
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Qy 693 ccttaccctcctgtgtggtggcggcggcggcggcggcggcggcggcggcggcggcggc 752
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Qy 753 agaagccagcggggcattcagggagctcagagcaggaagaaatggtccttgaggtgga 812
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Qy 813 gctaaagcctcccatccctcgtgtgagctgtcagtggtgtcagaaacagctgtgtgc 872
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Qy 873 tccctgccaacatccctgtgaggtggaagagataagtgctgtggtcttgatagcttcgt 932
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Qy 933 cggagaccagtgacatctgtcagcgaacggtcaltccacgcttccctacccagggcgg 992
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Qy 993 ttctgcatcatgtctacatccagcccaacacagatgtccatcttlttgaggtgtgat 1052
Db 1031 CAGCTCAATAAGATTTATATACCTATATATGCTACTATATATATATATGAACTGTGAT 1090
Qy 1053 atgagcagagcaacagtgagccccaacacagagagatcctcttgaggtgtcaacctgtg 1112
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Qy 1113 tccctgccaacagcctctcagccagccacatccgcccacacagctgcagcagccctaa 1172
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Qy 1173 ctctgttcagcatgtccagcagacacactaagggtgtgtgtcctcaggaacccctgtcgtg 1232
Db 1211 TGTAGTAAAG-----CCGGGAACCTCTGAAATACATAGATTAATTAATGAAAAATTT 1264
Qy 1233 atgtcccaagctgtccctcctcctcctcctcctcctcctcctcctcctcctcctcct 1292
Db 1265 CCCTCCCTAAAGATCACTCCATGATTTAGACGGGAGACTGATGCTTAAGGCCAA 1324
Qy 1293 tgcctgagcgtgtgtcctcagccagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1352
Db 1325 TAAACAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1384
Qy 1353 tgaactcgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1410
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RESULT 2

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US-08-812-533-1
; Sequence 1, Application US/08812533
; Patent No. 5837514
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaoan
; TITLE OF INVENTION: TRAF2-Associated Kinase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,533
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..2259
; US-08-812-533-1

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Query Match 16.1%; Score 468; DB 2; Length 2994;

Best Local Similarity 59.3%; Pred. No. 1.2e-118; Matches 817; Conservative 0; Mismatches 553; Indels 6; Gaps 1;

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: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/032,476
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/890,854
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: T97-006-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2268 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-09-032-476-1

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Query Match      2.3%; Score 68.2; DB 4; Length 2268;
Best Local Similarity 48.3%; Pred. No. 7e-09;
Matches 264; Conservative 0; Mismatches 268; Indels 15; Gaps 2;

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QY 119 aagaatccggagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 178
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Db 103 CAGCAACAGGTGACGACATTCCTCAGCAAGTCCCGGAGAGCTTAGCCCCGGAAC 162
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QY 239 a-----agcttcgcagtgaggaagaaagggagggcagggcagaggtgcta 286
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Db 223 GCTGCCCGAGATGTCCTGAGGGGGATGCAAGACTTGGCGCCCAATGACCTGCCCTGTG 282
QY 287 atcatgagatagctgtccagtgagggagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 346
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Db 283 GCCATGGAGTACTGCCAAGGAGGAGATCTCCGGAAGTACTGMAACCACTTTGAGAACCTGC 342
QY 347 ttgcggcttcctgaagagaggttcctagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 406
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QY 467 gtggcggagggagggcagagcctcatatagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 526
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Db 463 CAAGGAGAGACAGAGCTTA---ATACACAAATATTGACCTTAGGATATGCAAGAGAGCTG 519
QY 527 gacgaatgtagaagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 586
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QY 587 tatgagc 593
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Db 580 CTGAGC 586

RESULT 8

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US-08-890-854-1
: Sequence 1, Application US/08890854
: Patent No. 6235512
: GENERAL INFORMATION:
: APPLICANT: Rothe, Mike
: APPLICANT: Cao, Zhaodan
: APPLICANT: R guler, Catherine
: TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 268 BUSH STREET, SUITE 3200
: CITY: SAN FRANCISCO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/890,854
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: T97-006-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2268 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-08-890-854-1

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Query Match      2.3%; Score 68.2; DB 4; Length 2268;
Best Local Similarity 48.3%; Pred. No. 7e-09;
Matches 264; Conservative 0; Mismatches 268; Indels 15; Gaps 2;

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QY 59 tggcactatgacgtctgtagggagggccactgacgtgtgtacaagagccgaac 118
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Db 43 TGGGAATGAAAGAGCGCCCTGGGACAGGGGGATTGGAAATGTCATCCGATGGACAT 102
QY 119 aagaatccggagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 178
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 CAGCAACAGGTGACGACATTCCTCAGCAAGTCCCGGAGAGCTTAGCCCCGGAAC 162
QY 179 cctgaggttcagtgagggaggtttgaggttcctgcgagagctgaaccacagatcgtg 238
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Db 163 CGAGAGCGGTGTGCTGCGTCCAGATCCAGATCAGAAAGCTGACCCCAATGTGTG 222
QY 239 a-----agcttcgcagtgaggaagaaagggagggcagggcagaggtgcta 286
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 GCTGCCCGAGATGTCCTGAGGGGGATGCAAGACTTGGCGCCCAATGACCTGCCCTGTG 282
QY 287 atcatgagatagctgtccagtgagggagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 346
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 283 GCCATGGAGTACTGCCAAGGAGGAGATCTCCGGAAGTACTGMAACCACTTTGAGAACCTGC 342
QY 347 ttgcggcttcctgaagagaggttcctagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 406
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Db 343 TGTGCTGTGGGAGAGTGCATCTCCTACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 402

```

[illegible]

APPLICANT: Mercutio, Frank
 APPLICANT: Zhu, Hengyi
 APPLICANT: Barbosa, Miguel
 APPLICANT: Li, Gian
 APPLICANT: Murray, Brian W.
 TITLE OF INVENTION: STIMULOS-INDUCIBLE PROTEIN KINASE
 TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 City: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/910,820
 FILING DATE: 12-AUG-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Makl, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 860098.413c1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 8:

Query Match	2.3%	Score 68.2;	DB 3;	Length 3966;
Best Local Similarity	48.3%;	Pred. No. 9.2e-09;		
Matches 264; Conservative	0;	Mismatches 268;	Indels 15;	Gaps 2

OY	59	tgagcactgctgacccctctgagcgcaaggcgccactcgcagctgctatcaaggcccgaaac	118
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OY	119	aagaaatcccgsgagagctgtctgcctgtaaaagctcttcaactcagccagcctatcggcgaccct	1708
Db	103	cagggaacaacaggtctgagcagattgtccatcaacgaagcgcggcgcaaggctcagcccccggaaac	1620
OY	179	ccctgagctcagcgctgagggagcttctgaggtccctcgcgagcgctgaaatcacaggaacatcgtg	2388
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OY	239	a-----agctcttcgcagctgtgaggaagaaacgggagcgacggcgaggaagtgctata	2866
Db	223	gctgcgccgagatgctccctcgaggggatttgcagaactctgtgcaccaatgacacctgcgccctctg	2828
OY	287	atcatatgagatactctccacagctgggagcgctctgtgagcgctgtctggaagcacccttgagaaacg	3466
Db	283	gcacatgaggtactctcccaaggagagagatctccggagagtaacctgaaaccagcttctggaaactgc	3422
OY	347	ctcgagcttctcgaaagagagatctcctagctgctgctgcgctgctgctgtgtgtgtgtgcatgaac	4066
Db	343	tggtgctctcgsgagagtgccatctccatcccttgctgtgagacattgtcctctgtgcgtatga	4022
OY	407	caacctgcgggaggaatgtgcatctgtccatccggagacatacaacctctggaaacatcatgycgctg	4666
Db	403	tacctctcatgaaacaacaaatcatcatcatccggatctctaaagccagaaacaatctgcttcgag	4622
OY	467	gtgggcgagggagggcgagagcatctataaagctgtctgaactctgggctgtcccgcaagctg	5266
Db	463	caagagagaaacggaggtca---atcacaaaaattatctgaccagagatatgtccaaaggcctg	519
OY	527	gaagatgatgagaaagcttgtttctgtctatagttaacagagaaatcaactgcacccctgacatg	5866
Db	520	gatacagggcagctctctgacatcatctgtgtggagccctctgtaacctgtgtcccaaggctata	579
OY	587	tatgagc	593
Db	580	ctgagc	586

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RESULT 13
US-09-222-734-1
Sequence 1, Application US/09222734A
Patent No. 6077701
GENERAL INFORMATION:
APPLICANT: Chu, Keling
APPLICANT: Pot, David
TITLE OF INVENTION: IKK-beta Regulates Transcription Factors
FILE REFERENCE: 12441,78080
CURRENT APPLICATION NUMBER: US/09/222,734A
CURRENT FILING DATE: 1998-12-29
EARLIER APPLICATION NUMBER: 09/215,131
EARLIER FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 60/068,954
EARLIER FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3966
TYPE: DNA
ORGANISM: Homo sapiens
US-09-222-734-1

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Query Match	2.3%	Score 68.2;	DB 3;	Length 3966;
Best Local Similarity	48.3%;	Pred. No. 9.2e-09;		
Matches 264; Conservative	0;	Mismatches 268;	Indels 15;	Gaps 2

[illegible]

RESULT 14
US-09-124-476-1
Sequence 1, Application US/09124476
Patent No. 6087169
GENERAL INFORMATION:
APPLICANT: MICHALOVICH, DAVID
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestlia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,476
FILING DATE: 29-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 97305868.8
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestlia, Paul P
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30498
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 775 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-124-476-1

Query Match 2.3%; Score 67.2; DB 3; Length 775;
 Best Local Similarity 48.1%; Pred. No. 7.6e-09;
 Matches 263; Conservative 0; Mismatches 269; Indels 15; Gaps 2;

QY 59 tggcactatgtagctgtaggagggccactgcccagtggtgtaagaagccgaac 118
 DB 215 TGGGAATGAAAGAGCGCTTGGGNCAGGGGATTTGGAATGTCCATCCGATGCAACAT 274
 QY 119 aagaatccggaggaggtgtgctgtaaggtctcaactcagccactatcgagacct 178
 DB 275 CAGGAACAGGTGAGCAGATTGCCATCAGCAGTCCGCGAGGCTCAGCCCGGAGAC 334
 QY 179 cctaggttcagtgaggaagttcaggtccctgagagctgtaacacacacacatctg 238
 DB 335 CGAAGAGCGGTGCTCCCTGAGATCCAGATCATGAGAAAGGCTGAGCCACCCCAATGTGCTG 394
 QY 239 a-----agctattcgcagtgaggaagaaaggagagcagcgaggaagtgcta 286
 DB 395 GCTCCCGAGATGTCCCTGAGGGGATGACAGAACTTGGCCCAATGATGACCTGCTG 454
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 QY 347 ttcgggtcttcagaggaagttcctagtggtgctgctgctgctgctgctgagc 406
 DB 515 TGTGCTGTGGGGAAGGTCCTCCTGACCTGCTGAGTGCATGATGCTGCTGCTGAGA 574
 QY 407 cacttgaggaggaatgtagctgtccatcggaacacaaactggaacatcatgagcctg 466
 DB 575 TACCTTCATGAAACAGATCATCATCGGATCTAAAGCCAGAAACATGCTGCTCAG 634
 QY 467 gtggcgagggagggcagagcatctataagctgtcagcttcagctgagggctgagcagctg 526
 DB 635 CAAGGAGAACAGAGTTA---ATACACAAATTTATTGACCTAGATATGCCAAGAGCTG 691
 QY 527 gacatgtagaagattgttctgtctatgtagtaagaagaaatcctgcaaccctgacatg 586
 DB 692 GATCAGGCGAGCTTTTGACATCATTTGCTGGGANNCCGACGATGCTGCGCCAGAGCTA 751
 QY 587 tatgagc 593
 DB 752 CTGGAGC 758

RESULT 15
 US-09-577-796A-1
 Sequence 1, Application US/09577796A
 Patent No. 6316239
 GENERAL INFORMATION:
 APPLICANT: MICHALOVICH, DAVID
 TITLE OF INVENTION: NOVEL COMPOUNDS
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESS: Ratner & Prestia
 STREET: P.O. Box 980
 CITY: Valley Forge
 STATE: PA
 COUNTRY: USA
 ZIP: 19482

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/577.796A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/124,476
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F
 REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-30498
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 775 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-577-796A-1

Query Match 2.3%; Score 67.2; DB 4; Length 775;
 Best Local Similarity 48.1%; Pred. No. 7.6e-09;
 Matches 263; Conservative 0; Mismatches 269; Indels 15; Gaps 2;

QY 59 tggcactatgtagctgtaggagggccactgcccagtggtgtaagaagccgaac 118
 DB 215 TGGGAATGAAAGAGCGCTTGGGNCAGGGGATTTGGAATGTCCATCCGATGCAACAT 274
 QY 119 aagaatccggaggaggtgtgctgtaaggtctcaactcagccactatcgagacct 178
 DB 275 CAGGAACAGGTGAGCAGATTGCCATCAGCAGTCCGCGAGGCTCAGCCCGGAGAC 334
 QY 179 cctaggttcagtgaggaagttcaggtccctgagagctgtaacacacacacatctg 238
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 QY 239 a-----agctattcgcagtgaggaagaaaggagagcagcgaggaagtgcta 286
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 QY 287 atcatgagtagctgtccagtgaggagcctgtagcgctgctggaagccctggaacagc 346
 DB 455 GCCATGGAGTCTGCCAAGAGAGATCTCCGAAATGACTGACCCGATTGAGAACTGC 514
 QY 347 ttcgggtcttcagaggaagttcctagtggtgctgctgctgctgctgctgagc 406
 DB 515 TGTGCTGTGGGGAAGGTCCTCCTGACCTGCTGAGTGCATGATGCTGCTGCTGAGA 574
 QY 407 cacttgaggaggaatgtagctgtccatcggaacacaaactggaacatcatgagcctg 466
 DB 575 TACCTTCATGAAACAGATCATCATCGGATCTAAAGCCAGAAACATGCTGCTCAG 634
 QY 467 gtggcgagggagggcagagcatctataagctgtcagcttcagctgagggctgagcagctg 526
 DB 635 CAAGGAGAACAGAGTTA---ATACACAAATTTATTGACCTAGATATGCCAAGAGCTG 691
 QY 527 gacatgtagaagattgttctgtctatgtagtaagaagaaatcctgcaaccctgacatg 586
 DB 692 GATCAGGCGAGCTTTTGACATCATTTGCTGGGANNCCGACGATGCTGCGCCAGAGCTA 751
 QY 587 tatgagc 593
 DB 752 CTGGAGC 758

Wed May 15 09:30:46 2002

us-09-582-397a-3.rni

Page 11

Search completed: May 14, 2002, 17:31:45
Job time: 18698 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2002, 18:59:45 ; Search time 5236.03 seconds
(without alignments)
7501.130 Million cell updates/sec

Title: US-09-582-397A-3
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Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	777.2	26.7	809	10	BG076123 H3155H09-3
2	630.2	21.7	754	9	AV306791 AV306791
3	559.4	19.2	591	9	AM558201 10291H07-
4	548.2	18.8	851	10	BM051210 603634157
5	546	18.8	565	9	A1596282 uk24d10.x
6	531.2	18.3	2982	11	AK004649 Mus muscu
7	522	17.9	541	9	A1596210
8	516.2	17.7	908	10	BF102233 601752535
9	515	17.7	1031	10	BG754709 602714467
10	513	17.6	532	10	BG092901 mac20e05.
11	493	16.9	838	10	BM051314 603634307
12	491.6	16.9	540	9	A1155175 uc82h09.r
13	489.2	16.8	537	9	BB764205 BB764205
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17	475.2	16.3	656	10	BG248299 602400335

18	468.4	16.1	491	10	BF471509	BF471509 UI-M-BH3-
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22	446.6	15.3	476	9	AA646565	AA646565 ve46803.r
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25	428.4	14.7	558	10	BF073571	BF073571 220312 MA
26	423	14.5	524	9	BB766474	BB766474 BB766474
27	422.8	14.5	871	9	AL553975	AL553975 AL553975
28	412.6	14.2	457	9	A1050632	A1050632 ub38d03.r
29	409.2	14.1	476	10	BG091083	BG091083 mac20e05.
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36	342.8	11.8	414	9	A1663156	A1663156 uk23e02.y
37	335.6	11.5	354	9	AA798649	AA798649 vw34C05.x
38	334.4	11.5	451	9	A1663235	A1663235 uk24d10.y
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40	329.6	11.3	616	9	BE200581	BE200581 FK87e08.x
41	325.6	11.2	474	9	AW175691	AW175691 QV0-BT004
42	324.4	11.1	574	10	BI884083	BI884083 fm99d06.y
43	312.4	10.7	562	10	BF191384	BF191384 238954 MA
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ALIGNMENTS

RESULT 1
LOCUS BG076123 809 bp mRNA linear EST 26-JAN-2001
DEFINITION H3155H09-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3155H09 3', mRNA sequence.
ACCESSION BG076123
VERSION BG076123.1 GI:12558692
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka
T.S., Carter, M.G. and Ko, M.S.H.
TITLE Verification and Initial Annotation of NIA mouse 15K cDNA clone set
JOURNAL Unpublished (2001)
COMMENT Contact: George J. Kargul

National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnaelg@sun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit <http://ligsun.grc.nia.nih.gov/cDNA/15k.html> for details.
Plate: H3155 row: H column: 09
Seq primer: -21M13 Forward
High quality sequence stop: 809
POLY-A-yes.

FEATURES

source

Location/Qualifiers
1. 809
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/strain="C57BL/6J"
/db_xref="nia:EST:H3155H09-3"
/db_xref="taxon:10090"
/clone="H3155H09"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA libraries"
/lab_host="DH10B"

/note="Vector: pSPORT1; Site-1: SalI; Site-2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extreme embryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dt)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978.

BASE COUNT 203 a 186 c 228 g 192 t
ORIGIN

Query Match 26.7% Score 777.2; DB 10; Length 809;
Best Local Similarity 98.3%; Pred. No. 7,2e-165;
Matches 796; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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QY 2143 atccatcagaaggttcataagagcttcacacgacagatgctcagctcctgggggtt 2202
DB 749 ACTCATCGAAGGTTACATAGAGCTTCATGGCACAGATGCTAGCTCCCTGGGGGT 690
QY 2203 ccaagagcctcagaagacataagaacatcatatgacccctcactgtaagacaa 2262
DB 689 CACAAGGCACTCAGAAAGCAATGAAACATTTGTAACCTTACACTGTAGACAA 630
QY 2263 ttcagaggaagttcgttgcatactcactcactcctcctctgacatgacatg 2322
DB 629 TTCAGGGCAAGTTCGTGCTCATCTACAGCTACCTCCCTCATTTGCCATTTG 570
QY 2323 gccaaacactgagcttacttacttacttacttacttacttacttacttacttactt 2382
DB 569 GCCAACAACATGACATTAATCTTGTACTGCTCTTGGGAAGCAGCTAGACAGGCTCT 510
QY 2383 ggcacatcccaagcagatcatcagaagagacatgagctacacagccttaacaaga 2442
DB 509 GGCATCCCAAGCAGATCTACAGAAGAGCCATCGGCTACCAAGCCTTATCAAGCA 450
QY 2443 ccaagactgttcttcttacttacttacttacttacttacttacttacttacttactt 2502
DB 449 CCAAGACTGTTCTCTCACCAGGCTCTGAGGCTGTGTTGGAAGAAAGAGCTCAG 390
QY 2503 cccctcagcgttgcacttccagacagacagacatcctcgtggttctcctgctc 2562
DB 389 CCTCTCAGGCTCTGACTTCCCAAGACAGAGCGATGCTGTGCTTCTCTGCTC 330
QY 2563 tccagagtgatgacagaatgctatcttctgcttctcgtgctgcttctcctgagt 2622
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QY 2623 ccccatccctgagctcaggaaccccaagcgcctctgctgcttgccttagatgac 2682
DB 269 CCCCAT-CCCTGGGCTCAGGCAACCAACAGGCGCCCTGTGCTTGTCTAGATGAC 211
QY 2683 ctgcagtgagaagtggtggtgagtgactacgtgctgcttgccttagatctcctga 2742
DB 210 CGCATTGAGAAAGTGGGTGGTGAAGCTAGCTGCTGCTTGAAGATTCCTTGA 151
QY 2743 cctttctcagagacgcttggttcttaagaagacgctgctcagtatcaacacagcgat 2802

DB 150 CCTTTTCGCGAAGACGCTTGTTCTAAGAAACAGCTGTCAGTATCAACACAGCCAT 91
QY 2803 gtaactgagcagatgttggaaacccaaagtcttaagagagacagcctgacacctt 2862
DB 90 GCTAACTGAGCAGATGTTGGAACCAAGTCTTAAGGAGAGCAGGCTCACCCTTACG 31
QY 2863 acatgataataatcagccttctgtt 2892
DB 30 ACATGATTAATATCATGCTTTCTGT 1

RESULT 2
AV306791 754 bp mRNA linear EST 31-AUG-2001
LOCUS AV306791 RIKEN full-length enriched, 8 days embryo Mus musculus
DEFINITION cDNA clone 5730546107 3', mRNA sequence.
ACCESSION AV306791
VERSION AV306791.2 GI:15405972
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 754)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koyama, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, T., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Nov 10, 1999 this sequence version replaced gi:6339305.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayashizaki, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Yamanaka, T., Kiyosawa, R., Kondo, S., Saito, T., Shingawa, A., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Funct. Genomics 2 pre, 172-186 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Location/Qualifiers

FEATURES

ligation mixture by chemical method. The library was constructed by Xiaohong Wang and Yulan Piao."

BASE COUNT 150 a 141 c 171 g 129 t

ORIGIN

Query Match 19.28; Score 559.4; DB 9; Length 591;
Best Local Similarity 98.7%; Pred. No. 1e-115;
Matches 585; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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Db 591 TCCTCTGGCCATT-GCCATTGGCCCAACAACTAGCATTACTGCTCTGGG 533
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|||||
Db 532 AACGAGTAGGAGGAGGAGCTCGGCCATCCAGGAGATCTACAGAGAGAGCATGGG 473
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|||||
Db 472 GCTACACAGCCTTATCAACAGACCAAGACTGTTCTTCACCCAGGCTCTGAGGTCT 413
QY 2480 ggtcttgaaagaaagagcctcagcctcagccttgcagctccagagacagagca 2539
|||||
Db 412 GGTCTTGGAAGAAAGAGGCTCAGCCCTCTCAGCTCTGCACTTCCAGAGCAAGCAGCG 353
QY 2540 tctctctgagctctcctctcctcagaggtgctgagatcagaatgcttacttctgt 2599
Db 352 TCTCTGTGGCTTCTCCTGCTCTCCAGGAGTGTGATCAGATGCTTATCTGTGTTGT 293
QY 2600 ttccttgctgttctctgagtggtcccaaccctgctcagcagcaaccacaaagcc 2659
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Db 292 TTCTCTGTGGCTTCTCCTGAGTGTGCCATCC-CTGGCTCAGGCAACCCACAAACGGCC 234
QY 2660 ctctgctgtgctgctagatgacacatcttctgaaaggtggttggagcttactgt 2719
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Db 233 CTCCTGTGGCTTCTCCTGAGTGTGCCATCC-CTGGCTCAGGCAACCCACAAACGGCC 174
QY 2720 ggtgcttgaggaatctccttgcaccttctcctcagaaagcgttggcttctaaagc 2779
Db 173 GGTGCTTTGAGGATCTCTCTGACCTTCTCCGAGGAGAGCTGGTCTTAAGAAACAGC 114
QY 2780 tggctgatacaacacagacacatgtaactgacagatcttgaacacacaaagtctaaag 2839
Db 113 TGGTCACTATCAACACACAGCCTGTAAGTGGAGCATGTTGGAACCCAAATCTCTAAAG 54
QY 2840 agagagcagagcctgacaccttcagacatggaataataacacgcttcttctgt 2892
Db 53 AGAGAGCAGAGCCTGACCTTCAAGACATGAATTAATACATGCGCTTTCTGT 1

RESULT 4 851 bp mRNA linear EST 07-NOV-2001
LOCUS BM051210
DEFINITION 603634157F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:5424662 5',
mRNA sequence.
ACCESSION BM051210
VERSION BM051210.1 GI:16780477
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
plate: LNCM186 row: a column: 15
High quality sequence stop: 817.

FEATURES
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Location/Qualifiers
1..851
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/clone_1id="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pORF7; site: 1; XhoI; site: 2; EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library. |"

BASE COUNT 168 a 203 c 298 g 162 t

ORIGIN

Query Match 18.8%; Score 548.2; DB 10; Length 851;
Best Local Similarity 80.8%; Pred. No. 3.5e-113;
Matches 689; Conservative 0; Mismatches 158; Indels 6; Gaps 4;

QY 87 gggccactgacagtggtgacagagcccgaaacaaagaaatccggggaaggtgtgtgtaa 146
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QY 147 aggtcttaactcagccagctatcgagcctctctgaggttcaggtgaggttgaag 206
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Db 61 AGGTTTAAACACTTACAGTACCTGCGGCCCGAGAGTGCAGTGAAGGAGTTGAGG 120
QY 207 tcttcgagagctgatacagacagacatcgtgaagcttctcagtgagtgaggaagcagag 266
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Db 121 TCTCTGGAGACTGACACACAGCAACATCTCAACGCTTTGCGGTGAGAGACGGCG 180
QY 267 gcaagcagagaaagtgactaactcagagtaactgctcagtgagagcctctgagctgc 326
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QY 327 tgaagagccctgagaacacgcttgggcttctgagaaggggttctctgtgtgtgtgc 386
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QY 387 gttgtgtgtgcatgaaacacaccttgcgaggaatgcatgtcactcaggaacacaaac 446
Db 301 GTGTGTGGCCGATGACACCACTGCGGAGAGAGGAGCATTTGTGATCGGACATCAGC 360
QY 447 ctggaacacatagcgcctggtgaggaaggaaggaacacatctataagcttgcact 506
Db 361 CGGGGATCATATCGGCTCTGAGGAGAGGAGGAGAGACATCTACAACTGACAGACT 420
QY 507 tcggagctgcccgaagcctgagcagatgataagagttgttctgtctatagtaacagag 566
Db 421 TCGGCGCTGCCCGGAGCTGATGATGATGAAGTTCGCTCGCTTAAGGAGCTGAGG 480
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Db 481 AGTACGTGCAATCCGACATGATATAGCGGCGGTGCTTCCAAAGCCCGACCAAAAAAGC 540
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 Db 838 AGTCTTGGAGA 850
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 LOCUS AI596282/c
 DEFINITION U24010.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:196939 3, mRNA sequence.
 ACCESSION AI596282
 VERSION AI596282.1 GI:4605330
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 565)
 REFERENCE
 AUTHORS Marra,M., Haller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,Y., Person
 'B', Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurr,R., Rittler
 'E', Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterson,R. and Wilson,R.
 The Mashu-NCI Mouse EST Project 1999
 Unpublished (1999)
 CONTACT: Marra M/Mashu-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LIND; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:986679
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end
 Seq primer: custom primer used
 High quality sequence stop: 511.
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 /lab_host="DH10B"
 /note="Vector: pME18-FL3; Site 1: DraIII (CACTGTGCG);
 Site 2: DraIII (CAACCATGTC); 1st strand cDNA was primed
 with an oligo(dT) primer [ATGTGGCCCTTTTCTTTTCTTTT];
 double-stranded cDNA was ligated to a DraIII adaptor
 [GTGTGGCCCTGTCG], digested and cloned into distinct DraIII
 sites of the pME18-FL3 vector (5' site CACTGTGCG, 3' site
 CAACCATGTC). XhoI should be used to isolate the cDNA
 insert. Size selection was performed to exclude fragments
 <1.5kb. Library constructed by Dr. Sumio Sugano
 (University of Tokyo Institute of Medical Science).
 Custom primers for sequencing: 5' end primer
 CATTGCTTAAGCTGCG and 3' end primer
 CGACCTGACGCTCGAGACA."

BASE COUNT

142 a 136 c 160 g 127 t

ORIGIN
 Query Match 18.8%; Score 546; DB 9; Length 565;
 Best Local Similarity 98.9%; Pred. No. 1,1e-112;
 Matches 560; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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 Db 565 AACAACTAGCATTTACTTTGACCTGCTCTTGGGAAGCATAGACAGACTCTGGC 506
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 Db 445 AGACTGTTCTTCTCCACACCAGGCTCTGGAGCTGTGCTTTGGAAAGAAAGGCTCAGGCC 386
 QY 2506 tctcagccttgactctcccaagacagcagcagcctcctgtgctctcctcctcc 2565
 Db 385 TCTCAGCCTCTGCACCTTCCAGAGACAGAGCGCTCTGCTGTGCTTCTCTCTCTCC 326
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 RESULT 6
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 DEFINITION Mus musculus adult male lung cDNA, RIKEN full-length enriched
 library, clone:1200008B05;TANK-binding kinase 1, full insert
 sequence.
 ACCESSION AK004649
 VERSION AK004649.1 GI:12835968
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (Strain:C57BL/6J) adult male lung cDNA to mRNA,
 clone:1200008B05.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (sites)
 REFERENCE
 AUTHORS Carninci,P. and Hayashizaki,Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2 (sites)
 REFERENCE
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to


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QY 1841 taccagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcag 1900
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QY 1901 caccctg 1906
DB 1999 CAGCTG 2004

RESULT 7
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DEFINITION UK23602.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
ACCESSION A1596210
VERSION A1596210.1 GI:4605258
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 541)
AUTHORS Maira,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stepheo,M., Theising,B., Allen,M., Bowers,T., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schuck,R., Ritzer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson R.
TITLE The Washu-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Maira W/Washu-NCI Mouse EST Project 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone was previously sequenced on the 5' end only, this new data is from the 3' end
Seq primer: custom primer used
High quality sequence stop: 493.
Location/Qualifiers
1. 541
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/note="Vector: pME18S-FL3; Site 1: DraIII (CAGCTGTG); Site 2: DraIII (CAGCATGTG); 1st strand cDNA was primed with an oligo(dT) primer (ATGTGGCCCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TTGTGGCTTCTG); digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (3' site CAGCTGTG, 3' site CAGCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCCTCTTAAGAGCTGCG and 3' end primer

REFERENCE
1 (bases 1 to 588)
NIH-MGC <http://mgc.ncl.nih.gov/>.

529 cgaatgtagaagattgtttctcgtctatggtacagagaatacctgcacccatgata 588
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Db 421 ATTCCTGGACACATCCTGGAGGTGGAGACGAGATGATGCTGGGGCTTATACAGTCTCTT 480

QY 931 cgcgagaccagtgacattctcagcagcaagtgatccacgtctcttccacc 984

Db 481 CGGGAGACACAGTACATCTTCAGGACGAGGTC--TCCAGCTTTCCCTACCC 533

RESULT 15

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DEFINITION 602765743F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4907890 5', mRNA sequence.

ACCESSION BG831664

VERSION BG831664.1 GI:14179251

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mhc.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at:
http://image.jhmi.gov
Plate: LLCMI813 row: e column: 11
High quality sequence stop: 712.
Location/Qualifiers

FEATURES

source

1. 720

/organism="Homo sapiens"

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/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library. |"

BASE COUNT 173 a 201 c 222 g 124 t

ORIGIN

Query Match 16.5%; Score 481.2; DB 10; Length 720;

Best Local Similarity 81.7%; Pred. No. 4.5e-98;

Matches 595; Conservative 0; Mismatches 123; Indels 10; Gaps 3;

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QY 1175 ctgttcagcatgtccagcaacacactaagggtcgcttcaggaagccctctgcat 1234

Db 62 CTCCTCAGCAGACGCCATC-----CCTAAGGGGCTGGGCTTCAGAGGACCTCGCTGAGC 115

QY 1235 gtcccaaggtcgctccctaaagtgacctacagcgcgattacagcacagctaaagggtg 1294

Db 116 GTCCG-AAAGTGTCTCCCAAAAGTGACCTCGACGGCGGATTAACAACATGCCAAAGGCGTG 174

QY 1295 ctggagcgtcggtacacagccctgtggtgctggtcggtcgtggtgacagagcggtg 1354

Db 175 TTGGGCGCGGCTTACAGAGCCCTGCGGCTGGACAGGGCCCTGCTGGATGGCAGAGACTA 234

QY 1355 atgttcgggggttaccattgggtctcctggaggtgcttcaggaacagtgccagcaagacactg 1414

Db 235 ATGTTTCGGGGGCTGCATGGGTGATGAGAGTGTCTCCAGGCCACATGACAGAGACTGTG 294

QY 1415 gaagtcacagcaagaccctcctctactcctggcagcagcctggtgcaactggaaggtcagc 1474

Db 295 GAAGTGCAGAGCAATCCCTCTCTACTCTCAGACAGCAGCCTGGGAACGTGAGAGCTTCAGC 354

QY 1475 agtggatcgggtgtgctgtcagctcaggaagcaagaggaagcagagctaaagacccag 1534

Db 355 AGCGTGGCTGAACGCTTGATTCAGAGACTGAAAGGCGCTGCAGACTGAGTCCAG 414

QY 1535 ctgcagactctcagagatcctgtcttaaatgttcccaaatgtccagaaacccaag 1594

Db 415 CTGGGAGCTCTAGCGGAGAGTCTCTCCAGATGCTCCCAAAATATACAGGAGACCCAGAG 474

QY 1595 agcctgagctgtctggtggaagcctttaaagaaccgggagcagattcagagataac 1654

Db 475 AGCTTGACAGAGCCGAACCGGAGCTGTGMAAGCGGGGATCAGGTACATGANG--AC 531

QY 1655 aaagtatcagaagatcagttgttggagaagatgcaactcaactcaaacagctc 1714

Db 532 AGAAGCATCCAGCATGATTCAGTGTGTTGGACAGATGACTTCTATCAAAACAGTTG 591

QY 1715 aagaatccagatgagccagagctcagctacatgaaatgagagagatccacagctgcat 1774

Db 592 AAGAAGTCTAGAGATGAGCCAGGGCTTGCTTACACAGAGAGAGATTCACAGCTGAT 651

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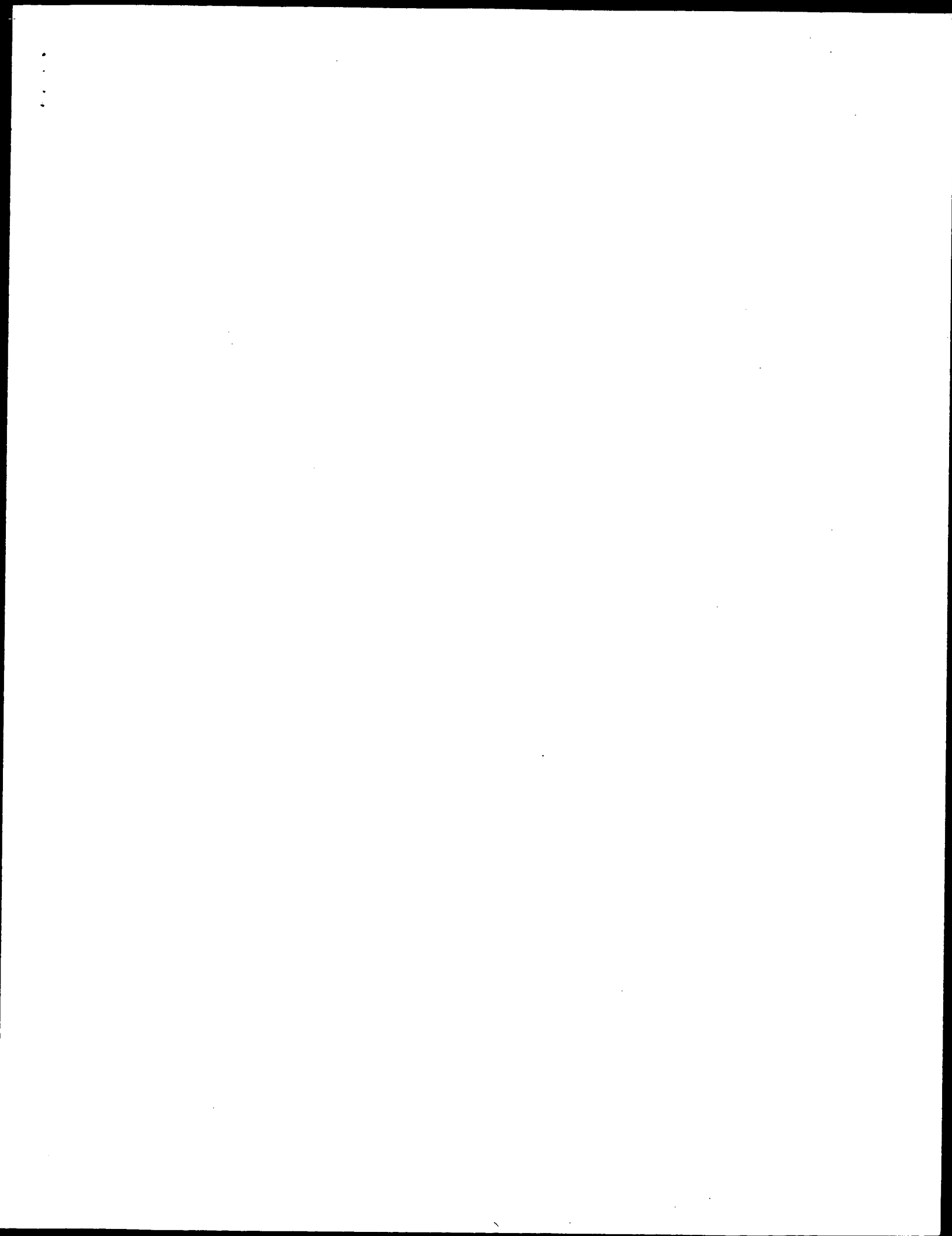
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QY 1835 cagagctta 1842

Db 712 CAGAAATA 719

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Job time: 15500 sec



GenCore version 4.5
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OW protein - protein search, using sw model

Run on: May 14, 2002, 19:14:54 ; Search time 103.46 Seconds
(without alignments)
769.763 Million cell updates/sec

Title: US-09-582-397A-4

Perfect score: 3726
Sequence: 1 MQSTNTYLMHTDDLLGCGAT.....LQDNRLIERLRHVPAPDV 717

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3726	100.0	717	21	AAAB01980 Murine I-kappa-B k
2	3712	99.6	717	21	AAAY80279 Murine I kappa B k
3	3102.5	83.3	716	21	AAAY3676 Amino acid sequenc
4	3102.5	83.3	716	21	AAAB01979 Human I-kappa-B k1
5	3100.5	83.2	716	21	AAAY3682 Amino acid sequenc
6	3098.5	83.1	716	21	AAAY3683 Amino acid sequenc
7	3097.5	83.1	716	21	AAAY3680 Amino acid sequenc
8	3096.5	83.1	716	21	AAAY3679 Amino acid sequenc
9	3093.5	83.0	716	21	AAAY3681 Amino acid sequenc
10	1660	44.6	729	19	AAAM60724 Human TR2 protein
	1660	44.6	729	20	AAAW9273 Human TR2 (TRAF2-a

12	1660	44.6	729	21	AAAY44240
13	1660	44.6	729	22	AAAE07905
14	1660	44.6	729	22	AAAB65601
15	1647	44.2	729	21	AAAY80280
16	1297.5	34.8	324	21	AAAB28859
17	1146.5	30.8	711	22	AAAB53265
18	694	18.6	254	22	AAAM25643
19	626.5	16.8	1214	21	AAAY79152
20	557	14.9	129	22	AAU17258
21	453	12.2	148	22	AAU17243
22	439.5	11.8	1007	21	AAAB6880
23	437.5	11.7	756	19	AAAY45097
24	437.5	11.7	756	20	AAAY43247
25	437.5	11.7	756	20	AAAY24051
26	437.5	11.7	756	20	AAAY14515
27	437.5	11.7	756	20	AAW96158
28	437.5	11.7	756	20	AAW82499
29	437.5	11.7	756	20	AAW86163
30	437.5	11.7	756	20	AAW81563
31	437.5	11.7	756	20	AAW81566
32	437.5	11.7	1005	21	AAW84882
33	436.5	11.7	756	19	AAW56328
34	399	10.7	799	21	AAW9153
35	387.5	10.4	741	12	AAW71288
36	356.5	9.6	745	19	AAW56329
37	356.5	9.6	745	20	AAW82498
38	356.5	9.6	745	20	AAW81562
39	356.5	9.6	745	20	AAW81565
40	352.5	9.5	745	20	AAW24052
41	352.5	9.5	745	20	AAAY14516
42	352.5	9.5	745	20	AAW96157
43	352.5	9.5	745	20	AAW86164
44	352.5	9.5	745	22	AAW67437
45	352.5	9.5	745	22	AAW67616

ALIGNMENTS

RESULT	ID	Score	Description
1	AAAB01980	3726	Murine I-kappa-B kinase (IKK-1).
2	AAAB01980	3712	Murine I-kappa-B kinase; IKK-1; murine; serine/threonine kinase; NF-kappa-B; nuclear factor kappa-B; inflammation; immune disorder; TRAF molecule; I-TRAF related disorder; antiinflammatory; immunostimulatory.
3	AAAB01980	3102.5	Mus sp.
4	AAAB01980	3102.5	WO200024908-A1.
5	AAAB01980	3102.5	04-MAY-2000.
6	AAAB01980	3102.5	26-OCT-1999; 99WO-JP05916.
7	AAAB01980	3102.5	26-OCT-1998; 98JP-0304085.
8	AAAB01980	3102.5	(NISC-) JAPAN SCI & TECHNOLOGY CORP.
9	AAAB01980	3102.5	AKIRA S, Shimada T;
10	AAAB01980	3102.5	WPI, 2000-350748/30.
11	AAAB01980	3102.5	N-PSDB; AAA52449.
12	AAAB01980	3102.5	Novel I-kappa-B kinase, IKK-1, capable of activating transcription
13	AAAB01980	3102.5	factor NF-kappa-B to inhibit expression of gene relating to immune
14	AAAB01980	3102.5	response, useful in drug compositions to treat inflammation and improve

PT Immune response mechanism -
 XX
 XX Claim 1; Fig 3; 52pp; Japanese.
 PS
 CC This sequence represents murine I-kappa-B kinase (IKK-1). IKK-1 is
 CC a serine/threonine kinase which can activate the transcription
 CC factor NF-kappa-B (nuclear factor kappa-B). The invention relates
 CC to the human and murine IKK-1 proteins (AA01979, AA01980), variants
 CC thereof, and to nucleic acids encoding human and murine IKK-1 (AA02448,
 CC AA02449). IKK-1 proteins are useful in drug compositions to treat
 CC inflammation and improve the immune response mechanism. They may also be
 CC used in preventing and treating diseases associated with the I-T-TRAP or
 CC TRAF molecule.
 CC
 XX Sequence 717 AA;
 SO

Query Match 100.0%; Score 3726; DB 21; Length 717;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOSTNTYLMHTDDLLGOGATASVYKARKKSGEVAVVFNASARYRPPDEVQVREFEYL 60
 DB 1 mstntnylwhtdlllggatalasvykarkksgevavvfnasaryrppdevqvefevlr 60
 QY 61 RINHONIVKLFVVEETGSRQKVLIMEYSSGSLISVLEDPENTFGISEEFVYLKRCV 120
 DB 61 rinhonivklfaveetgsrqkvlimeysssllsvledpentfgisseeflvylrcv 120
 QY 121 AGMNHLENGIYHRDIKPGNIMRLVGEQGSIYKLSDFGARKLDDDEKFEVSYGTEEYL 180
 DB 121 agmnhlrengiyhrdikpgnmlrvgeegsiyklstdfgarkldddekfsvygteeyl 180
 QY 181 HPDMTERAVLRKPOOKARVTVDMISIGVTLVYHATGSLPFPFGPPRNKEIWRITTE 240
 DB 181 hpdmteravlrkppokarvtdmislgtvlyhatgslpfpfgpprnkeiwritylte 240
 QY 241 KPAIGISTOKOENGLPFWMSLPTTGLSKGLONOLVPIANTILEVEDKCMGFDOFFA 300
 DB 241 kpagisltqkqngplfmslpttcrslnglqnlvpiantillevedkcmgfdoffa 300
 QY 301 ETSDLQFTVIVHFSLPQAVLHNYIHANMTATFLEAVVEQVTPKHOEYLFEGHPCV 360
 DB 301 etsdlqftvhlvhselpqavlhnyihantatfleaevqvtvprkheylfeghpcv 360
 QY 361 LEPSTSAOHIAHTAASSPLTFFSMSSDPKGLAFRDPALDVKFVPVVDLQADYSTAKV 420
 DB 361 lepsiisqhlhtaasspltlfmsadtpkglaftrdpaldvkvfpvvdldqadystakv 420
 QY 421 LGAGYQALMLARVLLDGOALMLRGLHWLVEYLODTCQOTLEVFTALLYGGSSIGTERES 480
 DB 421 lgaagyalmlarvllldgoalmrlglhwlvlelodtcqotlevftallyggssigteres 480
 QY 481 SSGSMPDVEERKEATELRTIQLTSELISKCSHWVETQSTLSQLEELLKNDQIHEDN 540
 DB 481 ssgsmpdveerkeatelrtiqltseliskcshwvetqstlsqleellkndqihedn 540
 QY 541 KSTOKIOCCDDKMHFTYKQFKSKMRPGLSTNEBQIHKLDKVNFSHLAKRLLOVFECEV 600
 DB 541 kstokioccddkmhftykqfkksmrpglstneeqihkldkvnfshlakra1lgvfcecv 600
 QY 601 QTVQSVLVTEGKRROVQRONHLIGHSVATCNSBARAOSLKNKIFQOLLDRASEO 660
 DB 601 qtvqsvlvtegkrrovqronhlighsvatcnsbaraoslknkifqollldrased 660
 QY 661 GAEVSPQPMAPHPGDPKDLVFHMOELCNDMKLAFDLQONNRLIERLHVPSAPDV 717
 DB 661 gaevspqpmaphpgdpkdvlvfhmocndmklaflqonnrlietlrvpsapdv 717

RESULT 2
 AA080279
 ID AA080279 standard; Protein; 717 AA.

XX
 AC AA080279;
 XX
 DT 26-MAY-2000 (first entry)
 XX
 DE Murine I kappa B kinase-related kinase 1 SEQ ID NO:2.
 XX
 KW Mouse; murine; I kappa B kinase-related kinase; IKK-1; IKK-2;
 KW protein kinase; immunomodulatory; antiinflammatory; antimicrobial;
 KW cytosolic; autoimmune; inflammatory; infection; neoplastic disease.
 OS Mus sp.
 XX
 PN WO200008179-A1.
 XX
 PD 17-FEB-2000.
 XX
 PF 04-AUG-1999; 99WO-US17578.
 XX
 PR 04-AUG-1998; 98US-0095269.
 PR 11-SEP-1998; 98US-009973.
 PR 05-FEB-1999; 99US-0118783.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Bird TA, Varca GD.
 XX
 DR WPI; 2000-195583/17.
 DR N-PDB; AA295275.
 XX
 PT Novel kappa B-kinase related kinases IKK-1 and IKK-2 used as molecular
 XX weight markers and in peptide fragmentation studies -
 PS Claim 13; Fig 3; 85pp; English.
 XX
 CC The present sequence represents murine I kappa B-kinase related kinase 1
 CC (IKK-1). IKK proteins have immunomodulatory, antiinflammatory,
 CC antimicrobial and cytostatic activities. IKK polypeptides can be
 CC used to express the proteins, and as probes to identify nucleic acids
 CC encoding proteins having kinase activity. IKK-1 and IKK-2 proteins and
 CC fragmented polypeptides are used for purifying proteins, e.g. to purify
 CC assurance agents to monitor shelf life and stability of binding partner
 CC proteins. They may also be used as research agents, e.g. in assays to
 CC determine protein kinase activity to identify novel molecules involved
 CC in signal transduction pathways, and to identify therapeutic compounds,
 CC to identify substances which interfere with the rate of substrate
 CC phosphorylation (such compounds would be useful for the treatment of
 CC autoimmune, inflammatory, infectious or neoplastic diseases), as
 CC molecular weight and isoelectric focusing markers, as controls for
 CC peptide fragmentation, identification of unknown proteins, e.g. by
 CC comparison with proteins in databases and for preparation of antibodies.
 CC The antibodies can be used in assays to detect the presence of the
 CC protein, and to purify the protein by immunoaffinity chromatography. The
 CC antibodies can also be used to block binding of the IKK polypeptides to
 CC their binding partners.
 CC
 XX
 SO Sequence 717 AA;
 Query Match 99.6%; Score 3712; DB 21; Length 717;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 714; Conservative 1; Mismatches 2; Indels 0; Gaps 0;


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DB 121 asgmnhlrengivhrdtkpqnimrlyveegqslyklsdfgaarkloddexfvsygleeyl 180
OY 181 HPDMYERAVLRKPOOKAFQFVVDLMSIGVTLVHAATGSLPFIPIFGPRRNKEIMYRITTE 240
DB 181 hpdmyeravlrkpgqafvvtvdwlslygtlyhaatgsplfpfpgprnrnkemlyritte 240
OY 241 KPAGATISGQKOBNGPLEMSYSLPTICRSLKGLQNDLVILANILEVEDKCKGPFQOFA 300
DB 241 kpagaatgskobngplemsyslpticrslsmglqndlvilnillevedckgpfqofa 300
OY 301 ETSDIQRTVIVHVSFPOAVLHHVYTHAHNTAIFLEAVYEONTPPKHOEYLFEGHPCV 360
DB 301 etsdiqrvtvvhvslpgevlnhvythahntaiflevayeqntvprkheylfeghpcv 360
OY 361 LEPSLSAONHTAHTAASSPILTFSSMSDTPKGLAFRDPAIDVPRKVPKVDLQADYSTAKGV 420
DB 361 lepslsaqnhahntaasspiltfssmsdtpkglafrdpaidvpkrvpkvdldqadystakgv 420
OY 421 LGAGYQALMLARVLDDGQALMLRGLHWLVEVLODTCQOTLEVTRTLALVYSSLGTERFS 480
DB 421 lgaqyalmlarvlddgqalmlrghwlvlevlodtcqqlvtrtalylsslgterfs 480
OY 481 SSGGMPDVORKEATELRTLTQTLSEILSKSHNVTETORSLSCLGEELKNRQIHEDN 540
DB 481 ssggmpdvorkeateltrtltqlselkschsnvteqrsiscjgeellknrdqhnedn 540
OY 541 KSIQKIQCCLDKMHFIYKQFKSRMRPGSLYNEEQIHKLDKVNFSHLAKRLQVFOBEVY 600
DB 541 ksqkqiccdldkmhfiykqfkksrmrpgslsyneeqihkldkvnfshlakrlqvfobecv 600
OY 601 QTVQVSLVTGKRMROVQRONHLHLIGHSVATCNSEARGAOSLUNKIPDOLLDRASEQ 660
DB 601 qtvqvsavltnghkrmrqvqrqgnhlhlgshvatcnsaargaeslnkifdqlldtraseq 660
OY 661 GAEVSPQPMAPHPGPPKDLVFMHQLCNDMKLLAFDLQDNRLIERLHRVPSAPDV 717
DB 661 gaevspqpmaphpqpdkdlvfmhgclndmkllafdlqdnrlrierlhrvpsapdv 717

RESULT 3
AAV93676
ID AAV93676 standard; Protein; 716 AA.
XX
AC AAV93676;
XX
DT 03-OCT-2000 (first entry)
XX
DE Amino acid sequence of a human IKK3 kinase.
XX
KW Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.
XX
OS Homo sapiens.
XX
PN WO200039308-A1.
XX
PD 06-JUL-2000.
XX
PE 24-DEC-1999; 99WO-JP07286.
XX
PR 24-DEC-1998; 98GB-0028704.
XX
PA (GLAXO) GLAXO WELLCOME KK.
XX
PI Takemoto Y, Sakai Y, Hashimoto Y;
XX
DR WPI; 2000-475700/41.
XX
DR N-PSDB; AAA47001.
XX
PT New IKK3 kinase protein and nucleotides encoding it, useful for
XX screening for IKK3 protein modulators for treating inflammation, e.g.
XX arthritis, atopic dermatitis or systemic lupus erythematosus

```

PS Disclosure; Fig 4; 102pp; English.

CC The present sequence represents a human IKK3 kinase protein. The protein
 CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
 CC useful for screening for agents with anti-inflammatory activity.
 CC Compounds which exhibit IKK3 kinase modulating activity may be used
 CC in formulating a treatment or prophylaxis of a disorder responsive to
 CC the modulation of IKK3 kinase activity in a mammal. The proteins,
 CC their variants or fragments, derivatives, analogues or cells expressing
 CC them can also be used as immunogens to produce antibodies against IKK3
 CC protein, which may further be used to locate the protein in tissues
 CC expressing that protein.

CC Sequence 716 AA;

Query Match 83.3%; Score 3102.5; DB 21; Length 716;
 Best Local Similarity 82.7%; Pred. No. 6.5e-271;
 Matches 596; Conservative 58; Mismatches 58; Indels 9; Gaps 4;

```

OY 1 MOSTNYLHTDLDLGGATFASVYKARNKSGEYVAVKVFNSASYRPPVQVREFEYL 60
DB 1 mgshtanylhtdldlggatfasyvyrnksgelyvavkvvfnstyslrppvqvreteyl 60
OY 61 RHNQNIYKLFVAVETGSRQKVLIMYCSGSLSLVLEDPENTFGLSEEFYLVLRVY 120
DB 61 rhnqniylkfvaveetgsrqkvlimeyccsgslslvleapnafglpedefylvlrcv 120
OY 121 AGMNHIRENGIYHRDKKPNINIRLVEEGQSYIKLSDFPAARKLDDDEFVSVGTTEYL 180
DB 121 agmnhlrengivhrdtkpqnimrlyveegqslyklsdfpaarkloddexfvsygleeyl 180
OY 181 HPDMYERAVLRKPOOKAFQFVVDLMSIGVTLVHAATGSLPFIPIFGPRRNKEIMYRITTE 240
DB 181 hpdmyeravlrkpgqafvvtvdwlslygtlyhaatgsplfpfpgprnrnkemlyritte 240
OY 241 KPAGATISGQKOBNGPLEMSYSLPTICRSLKGLQNDLVILANILEVEDKCKGPFQOFA 300
DB 241 kpagaatgskobngplemsyslpticrslsmglqndlvilnillevedckgpfqofa 300
OY 301 ETSDIQRTVIVHVSFPOAVLHHVYTHAHNTAIFLEAVYEONTPPKHOEYLFEGHPCV 360
DB 301 etsdiqrvtvvhvslpgevlnhvythahntaiflevayeqntvprkheylfeghpcv 360
OY 361 LEPSLSAONHTAHTAASSPILTFSSMSDTPKGLAFRDPAIDVPRKVPKVDLQADYSTAKGV 420
DB 361 lepslsaqnhahntaasspiltfssmsdtpkglafrdpaidvpkrvpkvdldqadystakgv 420
OY 421 LGAGYQALMLARVLDDGQALMLRGLHWLVEVLODTCQOTLEVTRTLALVYSSLGTERFS 480
DB 421 lgaqyalmlarvlddgqalmlrghwlvlevlodtcqqlvtrtalylsslgterfs 480
OY 481 SSGGMPDVORKEATELRTLTQTLSEILSKSHNVTETORSLSCLGEELKNRQIHEDN 540
DB 481 ssggmpdvorkeateltrtltqlselkschsnvteqrsiscjgeellknrdqhnedn 540
OY 541 KSIQKIQCCLDKMHFIYKQFKSRMRPGSLYNEEQIHKLDKVNFSHLAKRLQVFOBEVY 600
DB 541 ksqkqiccdldkmhfiykqfkksrmrpgslsyneeqihkldkvnfshlakrlqvfobecv 600
OY 601 QTVQVSLVTGKRMROVQRONHLHLIGHSVATCNSEARGAOSLUNKIPDOLLDRASEQ 660
DB 601 qtvqvsavltnghkrmrqvqrqgnhlhlgshvatcnsaargaeslnkifdqlldtraseq 660
OY 661 GAEVSPQPMAPHPGPPKDLVFMHQLCNDMKLLAFDLQDNRLIERLHRVPSAPDV 717
DB 661 gaevspqpmaphpqpdkdlvfmhgclndmkllafdlqdnrlrierlhrvpsapdv 717

Amino acid sequence of a human IKK3 kinase.
Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.
Homo sapiens.
WO200039308-A1.
06-JUL-2000.
24-DEC-1999; 99WO-JP07286.
24-DEC-1998; 98GB-0028704.
(GLAXO) GLAXO WELLCOME KK.
Takemoto Y, Sakai Y, Hashimoto Y;
WPI; 2000-475700/41.
N-PSDB; AAA47001.
New IKK3 kinase protein and nucleotides encoding it, useful for
screening for IKK3 protein modulators for treating inflammation, e.g.
arthritis, atopic dermatitis or systemic lupus erythematosus

```

Query Match	83.3%	Score 3102.5	DB 21	Length 716
Best Local Similarity	82.7%	Pred. No. 6,5e-271		
Matches 596	Conservative 58	Mismatches 58	Indels 9	Gaps 4
QY	1	MOSTNTYLHMTDDLGGQATASVYKARNKKSQGEVAVAVFNASASYRRPPEYQVREFEYLR 60		
Db	1	mgstanylwttdldlqgataasykarnkksqgelvaavvftttsylylpreyqvrefevir 60		
QY	61	RLNHQNVKRFKFAEETGSSROKVLIMEXCSSLSLSTVEDEPNTFGISEEFYLVLCVY 120		
Db	61	klnhqnlyvlkfaveeqgsrqlvlymexcssslstvspeenafiglpedeflavlrcvv 120		
QY	121	AGMNHILRENGIVHRDIPGNNIRLVEEGQOSIYKLSLDGAAKRLDDDEKFSVYGTPEYL 180		
Db	121	agmnhilrengivhrdipgnimrlvgeeqgslylktldgaareldddektvsyvgceyl 180		
QY	181	HPMYERAVLYRKRPQQAARFQVTDLMSSIGVTLYHAATGSLPIIPGGRRNNKEIMYRIITE 240		
Db	181	hpmlyeravlyrkpqaafqvtdlmsigvtllyhaatgslpifpfgprrnnkeimyltte 240		
QY	241	KPAQAISTQKQENGLEWYSFLPTCKRLSGLGNOLVPIIANTLVEEENKCMGCFQFOFRA 300		
Db	241	kpaqaistqkqenglewysflptckrlsglgnolvpiiantlveeenkcmgcfqfofra 300		

[illegible]

CC Compounds which exhibits IKK3 kinase modulating activity may be used
 CC in formulating a treatment or prophylaxis of a disorder responsive to
 CC the modulation of IKK3 kinase activity in a mammal. The proteins,
 CC their variants or fragments, derivatives, analogues or cells expressing
 CC them can also be used as immunogens to produce antibodies against IKK3
 CC protein, which may further be used to locate the protein in tissues
 CC expressing that protein.

CC Sequence 716 AA:

Query Match 83.2%; Score 3100.5; DB 21; Length 716;
 Best Local Similarity 82.5%; Pred. No. 9,8e-271;
 Matches 595; Conservative 59; Mismatches 58; Indels 9; Gaps 4;

QY 1 MOSTNYLWHTDLDGOGATASVYKARNKSGEVAVKFNASARYRPEVQVREFEYL 60
 DB 1 mgsstanylwhctdldlgogataasykarnksgelvaavkfnfntsylyrpevqvefevylr 60
 QY 61 RHNHONIVKLFVAVETGSGROKVLIMEYCSGSLSLVLEDPENTGSLSEEFVLVLCVY 120
 DB 61 kinhqivklfaveetgsgrokvlymecsagssllvleedpenafglpedefivlrcv 120
 QY 121 AGMNHIRENGIYHRDIPKCNIMKLVGEGOSITYKLSDFGAARKLDDDEKFSVYGTIEYL 180
 DB 121 agmnhirengiyhrdipkcnimrlyveeggsyikltdfgaareldddekfsvygteeyl 180
 QY 181 HPDMYERAVLRKPOOKAFEGYVDLWSIGVTLVYHAATGSLPFIPEGSPRNKEIMRTITE 240
 DB 181 hpdmyeravlrkpkafegvtdlwsigvtylhaatgslpfipegsprrnkeimryltte 240
 QY 241 KPAGALISGTOKEOENPLEWSYSLPTICRLSMGLOVLPILANILEVEDKCMGDFOPFA 300
 DB 241 kpagalagagqrengplewsylpticqslglsqjlvpllanilevegakcwgfdqfta 300
 QY 301 ETSDDLQRTVIVHFSLPQAVLHHVYTHAHTAIPLFLEAVYEQTNVTPKHOEYLFEGHPCV 360
 DB 301 etsddlqrvvvhvfhslsqavlnhlythahntaiflgeavhkhqtsvaprhqeylfeghlc 360
 QY 361 LEPSLSAQHIAHTAASSPILTFSSMSDTPKGLAFRDPALDVPKFKVPLQADYSTAKGV 420
 DB 361 lepsvaqhahantasspiltlftsa--lpxglafidpaldvprfkpvqlqadynakav 418
 QY 421 LGAGYQALMLARVLDGQALMLGMLHMLEVLDQTCQOTLEVTYRALLYGSLSGTERFS 480
 DB 419 lgaqygalmlaralldgqalmfghlmvmevlgatcrrtleavrtsllysslsigterfs 478
 QY 481 SSGGMPDVOEKREATELRRLQTLSEILSKSHNTETORSLSCLGEELIKNRDQIHEDN 540
 DB 479 svagrpelqelkaaaelrtrtlaevlarscqnltetqeslslslnreljvksrdyghed- 537
 QY 541 KSIQKIOCCCLDKMHFIYKQFKKSRMRPGLSYNEOIHKIDKNFSLAKRLLOVPEGEV 600
 DB 538 rslqqlqcccldkmfiykfkksrmpglsgyneqinkldknfslakrllqvigecev 597
 QY 601 QTYQVSLVTHGKRMQVQARQNHMLIGHSVATCNSEARGAQSLELNKIFD---QLLLDR 656
 DB 598 qtyqslvthgkrmqyqarqnmlhlgshvatcnseargaqslslsklleeshqllqdr 657
 QY 657 ASFOGAEVSPQAPAHPRGDDPKDVLVHMOELCDMKLAFDLODNKRLIERLHRVPSAD 716
 DB 658 a--kgaqasppriapyrpsrkdlllhmqelcegmklasdlldnrlterlhrvpsappd 715
 QY 717 V 717
 DB 716 V 716

RESULT 6
 AAY93683
 ID AAY93683 standard: Protein; 716 AA.
 XX
 AC AAY93683;

XX 03-OCT-2000 (first entry)
 DT
 XX Amino acid sequence of a human IKK3 kinase mutant protein.
 DE
 XX
 XX
 KW Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.
 KM
 XX
 XX Synthetic.
 OS
 XX Homo sapiens.
 XX
 PN WO200039308-A1.
 XX
 XX 06-JUL-2000.
 PD
 XX
 XX 24-DEC-1999; 99WO-JP07266.
 PF
 XX 24-DEC-1998; 98GB-0028704.
 PR
 XX
 PA (GLAXO) GLAXO WELLCOME KK.
 XX
 DR Takemoto Y, Sakai Y, Hashimoto Y;
 XX WPI: 2000-475700/41.
 XX

PT New IKK3 kinase protein and nucleotides encoding it, useful for
 screening for IKK3 protein modulators for treating inflammation, e.g.
 PT arthritis, atopic dermatitis or systemic lupus erythematosus -
 PS Disclosure: Page 94-97; 102pp; English.

CC AAY93679-83 represent human IKK3 kinase mutant proteins. The IKK3 kinase
 CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
 CC useful for screening for agents with anti-inflammatory activity.
 CC Compounds which exhibits IKK3 kinase modulating activity may be used
 CC in formulating a treatment or prophylaxis of a disorder responsive to
 CC the modulation of IKK3 kinase activity in a mammal. The proteins,
 CC their variants or fragments, derivatives, analogues or cells expressing
 CC them can also be used as immunogens to produce antibodies against IKK3
 CC protein, which may further be used to locate the protein in tissues
 CC expressing that protein.

CC Sequence 716 AA:

Query Match 83.2%; Score 3098.5; DB 21; Length 716;
 Best Local Similarity 82.5%; Pred. No. 1.5e-270;
 Matches 595; Conservative 58; Mismatches 59; Indels 9; Gaps 4;

QY 1 MOSTNYLWHTDLDGOGATASVYKARNKSGEVAVKFNASARYRPEVQVREFEYL 60
 DB 1 mgsstanylwhctdldlgogataasykarnksgelvaavkfnfntsylyrpevqvefevylr 60
 QY 61 RHNHONIVKLFVAVETGSGROKVLIMEYCSGSLSLVLEDPENTGSLSEEFVLVLCVY 120
 DB 61 kinhqivklfaveetgsgrokvlymecsagssllvleedpenafglpedefivlrcv 120
 QY 121 AGMNHIRENGIYHRDIPKCNIMKLVGEGOSITYKLSDFGAARKLDDDEKFSVYGTIEYL 180
 DB 121 agmnhirengiyhrdipkcnimrlyveeggsyikltdfgaareldddekfsvygteeyl 180
 QY 181 HPDMYERAVLRKPOOKAFEGYVDLWSIGVTLVYHAATGSLPFIPEGSPRNKEIMRTITE 240
 DB 181 hpdmyeravlrkpkafegvtdlwsigvtylhaatgslpfipegsprrnkeimryltte 240
 QY 241 KPAGALISGTOKEOENPLEWSYSLPTICRLSMGLOVLPILANILEVEDKCMGDFOPFA 300
 DB 241 kpagalagagqrengplewsylpticqslglsqjlvpllanilevegakcwgfdqfta 300
 QY 301 ETSDDLQRTVIVHFSLPQAVLHHVYTHAHTAIPLFLEAVYEQTNVTPKHOEYLFEGHPCV 360
 DB 301 etsddlqrvvvhvfhslsqavlnhlythahntaiflgeavhkhqtsvaprhqeylfeghlc 360
 QY 361 LEPSLSAQHIAHTAASSPILTFSSMSDTPKGLAFRDPALDVPKFKVPLQADYSTAKGV 420

```

Db      361 lepsvaqhahnttaassplitfsta--ipkglafdpaldvbkfvpkvdldgadyntakgv 418
QY      421 LGAGYQALMLARVLLDGOALMLRGLHWLEVLQDTCQQTLEVRTALYLGSLSGTERPS 480
Db      419 lqagyalrlarallldggelmlfrglhwmevlgatcorrlervatcslllylsslsjterfs 478
QY      481 SSGSGMDVQERKEATLRLRLQTLSEILSKSHNVTETORSLSCEELKRNDOIHEDN 540
Db      479 svagrpelqelkaaaelrlrltlaevlsrscsnltetgeslslnrelvkardgvhed- 537
QY      541 KSIOKIOCCLDKMHFIYKQFKKSRMPGSLSYNEBOIHKIDKYNFSLHAKRLQIVQOEQV 600
Db      538 rsiqdgqcdldmnmfiykqfkksrmrpglgyneeqihkldkvnfshlaktllqvfgcecv 597
QY      601 QTYQVSLVTHGKRMRQVQRAQNHLLIGHSVATCNSEARGAQSINKTFD---QILLDR 656
Db      598 qkygaalvthgkrmrqvtrvhetrnlrlvgsvaacteaagvgeslskleeshqllqdr 657
QY      657 ASEGGAESVPPQMAPHPGDPKDLVFHMOELCNDMKLLAFDLDNNRLIERLHRVPSAD 716
Db      658 a--kgagaspplapypptrkdlldlmqelcegmklasdlldnnrlrlrinvrppdp 715
QY      717 V 717
Db      716 v 716

```

RESULT 7

AAV93680
ID AAV93680 standard; Protein; 716 AA.

AC AAV93680;

DT 03-OCT-2000 (first entry)

XX Amino acid sequence of a human IKK3 kinase mutant protein.

DE Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.

OS Synthetic.

OS Homo sapiens.

PN WO200039308-A1.

XX 06-JUL-2000.

PF 24-DEC-1999; 99WO-JP07286.

XX 24-DEC-1998; 98GB-0028704.

PA (GLAX) GLAXO WELLCOME KK.

PI Takemoto Y, Sakai Y, Hashimoto Y;

DR WPI; 2000-475700/41.

XX New IKK3 kinase protein and nucleotides encoding it, useful for

PT screening for IKK3 protein modulators for treating inflammation, e.g.

XX arthritis, atopic dermatitis or systemic lupus erythematosus

PS Disclosure: Page 82-86; 102pp; English.

XX AAV93679-83 represent human IKK3 kinase mutant proteins. The IKK3 kinase
CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
CC useful for screening for agents with anti-inflammatory activity.
CC Compounds which exhibit IKK3 kinase modulating activity may be used
CC in formulating a treatment or prophylaxis of a disorder responsive to
CC the modulation of IKK3 kinase activity in a mammal. The proteins,
CC their variants or fragments, derivatives, analogues or cells expressing
CC them can also be used as immunogens to produce antibodies against IKK3
CC protein, which may further be used to locate the protein in tissues
CC expressing that protein.

XX Sequence 716 AA;

Query Match 83.1%; Score 3097.5; DB 21; Length 716;
Best Local Similarity 82.5%; Pred. No. 1; Be-270;
Matches 595; Conservative 59; Mismatches 58; Indels 9; Gaps 4;

```

QY      1 MOSTTNYLMHDDLDGGATATAYKARKKSGEVAANKVENSASRYRPPPEYQREFFVL 60
Db      1 mgsstanylwhddldlggatasaykarkksgelvaakvfnlcsylrpreqvareffvl 60
QY      61 RLNHQNTYKFLAVETGSGRQKVLIMEYCSGSLSYLEDPEPTFGSEEFVLVLRQCV 120
Db      61 klnqnlkylflaveetgsrcqvlimeycassgslavleapenafigpedefvlvrcov 120
QY      121 AGMHRLRNGIVHNDIRPGNIMRLVGEQGSITKLSDFGAARKLIDDEKRVSYGIEEYL 180
Db      121 agmhrlrengivhndirpynlmrlvgeeqgslykltldfgaarellddekrtvsygyteeyl 180
QY      181 HPDWYERAVLRKPOOKAFGVTVDLMSIGVTLVHNAATGSLPFIPGGRRKKEIMYRTTE 240
Db      181 hpdwyeravlrkpgokafgvtrvdlmsigvtlvlynaatgslpfpipgprnkkeimyrllte 240
QY      241 KPAGASGTOKEQNGPLEWSYSLPTICRLSMGLQNDLVPLTIANILEVEEDKCGPQFPA 300
Db      241 kpagaagagatrenqngplewsylpticqlslglsqslvpllanllevegakcwgfdffa 300
QY      301 ETSIDLQRTVIVHVSLEPQAVLHNYTHAHNTIAFLFNAVTEQTNVTPKHQOYLFEGHPCV 360
Db      301 etsidlqrvtvvhvslsqavlhnythahntiaflfnavtktsvaprhqeylfeghlcvc 360
QY      361 LEPLSAOHIAHTAASSPLTFSSMSDTPKGLAFRDPALDPKVPFVVDLQADYSTRAGV 420
Db      361 lepsvaqhahnttaassplitfsta--ipkglafdpaldvbkfvpkvdldgadyntakgv 418
QY      421 LGAGYQALMLARVLLDGOALMLRGLHWLEVLQDTCQQTLEVRTALYLGSLSGTERPS 480
Db      419 lqagyalrlarallldggelmlfrglhwmevlgatcorrlervatcslllylsslsjterfs 478
QY      481 SSGSGMDVQERKEATLRLRLQTLSEILSKSHNVTETORSLSCEELKRNDOIHEDN 540
Db      479 svagrpelqelkaaaelrlrltlaevlsrscsnltetgeslslnrelvkardgvhed- 537
QY      541 KSIOKIOCCLDKMHFIYKQFKKSRMPGSLSYNEBOIHKIDKYNFSLHAKRLQIVQOEQV 600
Db      538 rsiqdgqcdldmnmfiykqfkksrmrpglgyneeqihkldkvnfshlaktllqvfgcecv 597
QY      601 QTYQVSLVTHGKRMRQVQRAQNHLLIGHSVATCNSEARGAQSINKTFD---QILLDR 656
Db      598 qkygasivthgkrmrqvtrvhetrnlrlvgsvaacteaagvgeslskleeshqllqdr 657
QY      657 ASEGGAESVPPQMAPHPGDPKDLVFHMOELCNDMKLLAFDLDNNRLIERLHRVPSAD 716
Db      658 a--kgagaspplapypptrkdlldlmqelcegmklasdlldnnrlrlrinvrppdp 715
QY      717 V 717
Db      716 v 716

```

RESULT 8

AAV93679
ID AAV93679 standard; Protein; 716 AA.

AC AAV93679;

DT 03-OCT-2000 (first entry)

XX Amino acid sequence of a human IKK3 kinase mutant protein.

DE Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.

OS Synthetic.
 OS Homo sapiens.
 PN MO200039308-A1.
 XX
 XX 06-JUL-2000.
 PD
 PF 24-DEC-1999; 99WO-JP07286.
 XX
 XX 24-DEC-1998; 98GB-0028704.
 XX
 XX (GLAX) GLAXO WELLCOME KK.
 PA
 PI Takemoto Y, Sakai Y, Hashimoto Y;
 XX
 XX WPI: 2000-475700/41.
 DR
 XX
 PT New IKK3 kinase protein and nucleotides encoding it, useful for
 PT screening for IKK3 protein modulators for treating inflammation, e.g.
 PT arthritis, atopic dermatitis or systemic lupus erythematosus -
 XX
 PS Disclosure; Page 79-82; 102pp; English.

CC AAY93679-83 represent human IKK3 kinase mutant proteins. The IKK3 kinase
 CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
 CC useful for screening for agents with anti-inflammatory activity.
 CC Compounds which exhibit IKK3 kinase modulating activity may be used
 CC in formulating a treatment or prophylaxis of a disorder responsive to
 CC the modulation of IKK3 kinase activity in a mammal. The proteins,
 CC their variants or fragments, derivatives, analogues or cells expressing
 CC them can also be used as immunogens to produce antibodies against IKK3
 CC protein, which may further be used to locate the protein in tissues
 CC expressing that protein.
 CC
 XX
 SO Sequence 716 AA;

Query Match 83.1%; Score 3096.5; DB 21; Length 716;
 Best Local Similarity 82.5%; Pred. No. 2.3e-270;
 Matches 595; Conservative 58; Mismatches 59; Indels 9; Gaps 4;

QY 1 MOSTTYYLHHTDGLGQGTASTYKARKKSGEVAVKFNNSAYRPPVQYREYVR 60
 DB 1 mgtataylwhtdllgqgataasykarkksgelavawmftntslrprevyrefevlr 60
 QY 61 RLNHQNIKLFVAVETGSGRQKVLIMEYSSGSLSVLEDPENTFCLSEEFVLYRCV 120
 DB 61 klnhqnivklfaveetgsgrrqkvlimeysscsgllsvlespenafjlpedefivlrcv 120
 QY 121 AGNHLRENGIYHRDIKPGNIMRLVGEQSIYKLSDFGAARKLDDKRFVSYGTEEXL 180
 DB 121 agnhlrengiyrdrdkpknimrlvgeeqsiykltfdgaareldddefsvygeeyl 180
 QY 181 HPMYRVALRKPRQOKAFQVTDWISIGVLYHAATGSPFIPFGGPRRNKELMYITTE 240
 DB 181 hpmrvalrkrpqokafqvtdwlsigvlyhaatgsplfpfggprnrnkemlyitlte 240
 QY 241 KPAGASITQOKENGPRLENSYSPLTRCLSMGQNLQVLTNLNILEVEDKCMGPFQFPA 300
 DB 241 kpagalsagqrrengrplensyspltrclsqslqsgslvpllanlleveqakcwgffqfa 300
 QY 301 ETSIDILQRTFVIVFSLPQAVLHHVYTHAHNTAIFLEAVEYEQTNWTPKHQEYLFEGHPCV 360
 DB 301 etsidilqrtnvfvfslpqaavlhhvthahntaifgavhkhktsvaprneylfeghlc 360
 QY 361 LEPSSAIOHIAHTAASSPLTFLSMSSDTPKGLAFRPAIDVRFVVKVQLQDYSIAKAV 420
 DB 361 lepsvaqhiantassplltflsta--lpglaftdpaldvfkvpkvdldqadynakgv 418
 QY 421 LGAGYQALMLARVLLDGOALMLRGLHMLVLEVLQDTCCQOTLEVTPLALTLGSSIGTERPS 480
 DB 419 lgaqyqalrlarallldgqalmfrglhmlvmevlqatcrrtleavartslllysslsgrts 478

QY 481 SSGNPDYQERKEATRLRLOTLSLISKCSHNVTETORSLSCLGEELLNRPQIHEDN 540
 DB 479 svagprpelglkaaelrsrltlaevlsrscgnltetqesslnrelvrsrdvhd 537
 QY 541 KSIQKIOCCCLDKMHFTYQFKKSRMRPGLSTINEQIHLKDVNESHAKRLQYFQECV 600
 DB 538 tsigqigccldkmftlyqfkksrmpglgyneeqihkdvfnshlakrllyvqeev 597
 QY 601 QTYQSVLYTHGKRMROVQRAONHLHLIGHSVATCSFARGQESLNKLTED----QLLDR 656
 DB 598 qkyqaslythgkrmrvtvnetrhlrlvgcsvaactceqgyqeslsklllelsqllqdr 657
 QY 657 ASEGAEVSPQMAPHPGDPKDLVFMQELCNKMLAFDLDNNRILIERLHRVSPAD 716
 DB 658 a--kgagaspppiapyrptkdlillhmgelcegmklilasldldnrlterlrvpappd 715
 QY 717 V 717
 DB 716 v 716

RESULT 9

ID AAY93681 standard; Protein; 716 AA.

AC AAY93681;

DT 03-OCT-2000 (first entry)

DE Amino acid sequence of a human IKK3 kinase mutant protein.

KW Human; IKK3 kinase; IL-8 gene regulator; anti-inflammatory; immunogen.

OS Synthetic.

OS Homo sapiens.

PN WO200039308-A1.

PD 06-JUL-2000.

PF 24-DEC-1999; 99WO-JP07286.

PR 24-DEC-1998; 98GB-0028704.

PA (GLAX) GLAXO WELLCOME KK.

PI Takemoto Y, Sakai Y, Hashimoto Y;

DR WPI: 2000-475700/41.

PT New IKK3 kinase protein and nucleotides encoding it, useful for
 PT screening for IKK3 protein modulators for treating inflammation, e.g.
 PT arthritis, atopic dermatitis or systemic lupus erythematosus -

PS Disclosure; Page 86-90; 102pp; English.

CC AAY93679-83 represent human IKK3 kinase mutant proteins. The IKK3 kinase
 CC is an interleukin-8 (IL-8) gene regulator. The IKK3 kinase protein is
 CC useful for screening for agents with anti-inflammatory activity.
 CC Compounds which exhibit IKK3 kinase modulating activity may be used
 CC in formulating a treatment or prophylaxis of a disorder responsive to
 CC the modulation of IKK3 kinase activity in a mammal. The proteins,
 CC their variants or fragments, derivatives, analogues or cells expressing
 CC them can also be used as immunogens to produce antibodies against IKK3
 CC protein, which may further be used to locate the protein in tissues
 CC expressing that protein.
 CC
 XX
 SO Sequence 716 AA;

Query Match 83.0%; Score 3093.5; DB 21; Length 716;
 Best Local Similarity 82.4%; Pred. No. 4.2e-270;
 Matches 594; Conservative 59; Mismatches 59; Indels 9; Gaps 4;

QY 466 ALLYLSSLGTERFSSGSGMPDVOERKEATELRTLOTLSKSHNTEFORSLCL 525
 Db 479 vkyy-----eklmkn--leaaelgelsdhtkllrlsssgtletsqddslspg 529
 QY 526 GE--ELLNKDQIHEDKKSIOKIQCCDKMHFTYKOFKSRMRPGLSYNEQOIHKLKDVN 583
 Db 530 gsladawahqegctpkpkrneklqvllncmteluygfkdkkaerilayneeqihkfdkgk 589
 QY 584 FSHLAKRLLOVFOEECVQOTQVSLVTHGKRMROVQRAQNHHLIGHSVATCSEARGAQE 643
 Db 590 lyyhatkamchftdecvkkyeaflnkseewlrmlhrlkqlsltnqctfdeeevskyege 649
 QY 644 SLNKIFDQLLDR-ASEQGAESVSPQMAPRPGDPKDLVFMQELCNMKLAFDLQDN 702
 Db 650 ytnelgetlpqkmtfaassgikhtmtprlypsn-tlyvemtlgmkkllkeemegvvelaenn 708
 QY 703 RLIER 707
 Db 709 hiler 713

RESULT 11

AAW79273
 ID AAW79273 standard; Protein; 729 AA.

AC AAW79273:

DT 21-JAN-1999 (first entry)

DE Human T2K (TRAF2-associated kinase) protein sequence.

XX T2K protein; immunogen; transcriptional regulator; screening; human;

KM gene therapy; diagnosis; IkappaB kinase; NF-kappaB transcription factor;

XX drug development; TRAF2-associated kinase.

OS Homo sapiens.

PN US5837514-A.

XX 17-NOV-1998.

PE 07-MAR-1997; 97US-0812533.

PR 07-MAR-1997; 97US-0812533.

PA (TUL-) TULARIK INC.

XX Cao Z;

XX WPI; 1999-023452/02.

DR N-PSDB; AAV62697.

XX Recombinant or isolated nucleic acid encoding TRAF2-associated

PT kinase - which regulates inhibitors of NF-kappaB transcription

PT factors; useful as immunogen; for isolation of other transcriptional

XX regulators; in drug screening; and in gene therapy

PS Claim 1; Columns 9-16; 11pp; English.

XX This represents a T2K (TRAF2-associated kinase) protein belonging to

CC the family of IkappaB kinases. Cells containing a recombinant T2K nucleic

CC acid are used to produce the T2K protein which is useful as immunogen,

CC for isolation of other transcriptional regulators and in drug screening.

CC The T2K nucleic acid and corresponding antisense sequences, are useful

CC in gene therapy to modulate T2K expression, and its fragments are used as

CC probes and primers in diagnostic assays (hybridisation or amplification),

CC for identification of related sequences and to detect wild-type or mutant

CC alleles. The T2K nucleic acid can also be used to create transgenic

CC animals for studying the efficacy of candidate drugs. T2K binding agents

CC are useful in diagnosis, therapy and drug development, e.g. they can

CC activate, inhibit or alter T2K-dependent processes and activity of NF-

CC kappaB transcription factor.

SO Sequence 729 AA:

Query Match 44.6%; Score 1660; DB 20; Length 729;

Best Local Similarity 46.6%; Pred. No. 1.3e-140;

Matches 338; Conservative 130; Mismatches 227; Indels 30; Gaps 7;

QY 1 MOSTNYLWHTDDLLGOGATASVYKARNKSGEVAVKVFNSASYRRPEVOYREFEVL 60
 Db 1 mgetsnhlwlsdliggatanvfrgrhktgdlfalkfnlslfrpvdgmrefevlk 60
 QY 61 RLNHQIVKLVFAVEFTGSGKQKLVIMEYSSGSLSVLEDPEPTGOLSEEF-VVLRGV 120
 Db 61 klnkhivkflfaeettrhkwlmefpcpslylvleapnagylpesetflvldv 120
 QY 121 AGKNHLRENGIVHRDKRPGKIMRLVGEOSIYKILDFGARKLDDDEFVSYYGTEEL 180
 Db 121 ggmhlrengivhrdkrpgkimrlvgeosiykildfgarkldddefvsllygteel 180
 QY 181 HPDMYERAVLRLKPOKAFGVTVDLMSIGVLYHAATGSLPEFPGRRNKEIMVRIITTE 240
 Db 181 hpdmeyeravlrkphqkkygatvdlwslgvtlyhaatgslpfrpfgrrnkeimvrlitg 240
 QY 241 KPAKAISGTOKEOENGPLEMSYSLPTICRLSMGLOQNLVPLANILEVEDKCGFDQPA 300
 Db 241 kpsgaitsvgkkaengpildwsgdmpvscslsrglqvlltpvlnlleadqekcvgfdqfa 300
 QY 301 ETSDDLORTYTHVESLPQAVLHVYIHAHNTAIFLEAVYEONVTPKHQOYLFEGHPCV 360
 Db 301 etsdilhmythvtslqgmtnhkiylnsyntatlfelvykqklssngellvegrtlv 360
 QY 361 LEPSLSNOHIAHTAASSPLTLFSSMSDTPKGLAFRDPALDVPKVPKVDLQADYSTAKGV 420
 Db 361 lepgriaghrpkkteenplrfvareplnltgllye--klsrlvphrpyldgslasakel 418
 QY 421 LGAGYQALMLARVLLDGOALMLBGLHMLVEVLDDTCQQL-----EVTPT 465
 Db 419 tgvvcyacrtacllllyqelmrqgrlwllelddvetvhtkvevltldfclmtekt 478
 QY 466 ALLYLSSLGTERFSSGSGMPDVOERKEATELRTLOTLSKSHNTEFORSLCL 525
 Db 479 vkyy-----eklmkn--leaaelgelsdhtkllrlsssgtletsqddslspg 529
 QY 526 GE--ELLNKDQIHEDKKSIOKIQCCDKMHFTYKOFKSRMRPGLSYNEQOIHKLKDVN 583
 Db 530 gsladawahqegctpkpkrneklqvllncmteluygfkdkkaerilayneeqihkfdkgk 589
 QY 584 FSHLAKRLLOVFOEECVQOTQVSLVTHGKRMROVQRAQNHHLIGHSVATCSEARGAQE 643
 Db 590 lyyhatkamchftdecvkkyeaflnkseewlrmlhrlkqlsltnqctfdeeevskyege 649
 QY 644 SLNKIFDQLLDR-ASEQGAESVSPQMAPRPGDPKDLVFMQELCNMKLAFDLQDN 702
 Db 650 ytnelgetlpqkmtfaassgikhtmtprlypsn-tlyvemtlgmkkllkeemegvvelaenn 708
 QY 703 RLIER 707
 Db 709 hiler 713

RESULT 12

AAV44240
 ID AAV44240 standard; Protein; 729 AA.

XX AAV44240:

XX 28-FEB-2000 (first entry)

XX Human cell signalling protein-3.

DE Cell signalling protein-3; CSICP-3; cell proliferation; arteriosclerosis;

KM inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;

XX Addison's disease; multiple sclerosis.

XX OS Homo sapiens.
 XX XX
 XX Key Location/Qualifiers
 XX Modified-site 78
 XX /note= "Potential phosphorylation site"
 XX 96
 XX /note= "Potential phosphorylation site"
 XX 235
 XX /note= "Potential phosphorylation site"
 XX 239
 XX /note= "Potential phosphorylation site"
 XX 348
 XX /note= "Potential phosphorylation site"
 XX 373
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 XX /note= "Potential phosphorylation site"
 XX 682
 XX /note= "Potential phosphorylation site"
 XX 42
 XX /note= "Potential phosphorylation site"
 XX 455
 XX /note= "Potential glycosylation site"
 XX 614
 XX /note= "Potential glycosylation site"
 XX 9..238
 XX /label= "Signature_sequence"
 XX W0958558-A2.
 XX 18-NOV-1999.
 XX 13-MAY-1999; 99MO-US10567.
 XX 13-MAY-1998; 98US-0085343.
 XX 26-MAY-1998; 98US-0098010.
 XX (INCY-) INCYTE PHARM INC.
 XX Bandman O, Hillman JL, Lai P, Yue H, Tang YT, Patterson C;
 XX Baughn MR, Yang J;
 XX WPI: 2000-086432/07.
 XX DR N-PSDB; AA229224.
 XX Human cell signaling proteins useful for, e.g. diagnosing cell
 XX proliferative and inflammatory disorders
 XX Claim 1; Page 66-67; 90pp; English.
 XX
 XX The present sequence is cell signalling protein-3 (CSIGP-3) encoded
 XX by cDNA obtained from incyte clone 1250171 of LUNGEF703 library. It is
 XX expressed in reproductive, haematopoietic/immune and nervous
 XX tissues and is found to be homologous to serine/threonine protein
 XX kinase. Fragments of CSIGP encoding nucleic acid can be used as
 XX hybridisation probe for detecting CSIGP related sequences or allelic
 XX variants. Recombinant CSIGP can be produced in host cells by transforming
 XX them with genetically engineered vectors. Agonists or antagonists can be
 XX used in the treatment of cell proliferative and inflammatory disorders
 XX associated with decreased or increased CSIGP expression. CSIGP is used in
 XX the diagnosis, prevention and treatment of cell proliferative disorders
 XX like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
 XX disorders like AIDS, Addison's disease, multiple sclerosis, etc.
 XX
 XX Sequence 729 AA;

Query Match 44.6%; Score 1660; DB 21; Length 729;

Best Local Similarity 46.6%; Pred. No. 1,3e-140;
 Matches 338; Conservative 130; Mismatches 227; Indels 30; Gaps 7;

QY 1 MOSTNTYMTHTDGLGCGATASVTKARKKSGEVAAKVENASASRRPPEVQVREFFVL 60
 Db 1 mgsstnhlwlldslggatatanvfrghkktgdlfaikvfnfnisflrpdvqmfefevik 60
 QY 61 RHNHNIKLVAVEPTGSRKQVLMFECSSGSLVLEDEPNFGLSDEEFLVLCV 120
 Db 61 klnknlvklaleeettlnkvlimecpcgslytlvleepsnagylpseeflilvdv 120
 QY 121 AGMNHLENGIVHNDIKPNTMLVGEQGSIVKLSDFGAARKLDDKEKVSVYGTTEYL 180
 Db 121 gsmhlrenglvhndikpnmrlvgedgsvykltdfgareledgedqfvslygtceyl 180
 QY 181 HPDMTERAVLKKPOQKAFGVVDLWSIGVTLVHAATSSLPPIPGPRRNKEIMYRTTTE 240
 Db 181 hpdmyeravllkdkhqqkygatvdlwsigvtflyhaatgslypfrpgeprnrkemykiltg 240
 QY 241 KPAGASICTGKQENGLPMSVSLPITQRLSMGLQNLVPIANTLVEDEKCKGFOFFA 300
 Db 241 kpsgalisgvkaengplawsgdmpvscslsrqlvlllpvlaanlleadgexcwqldqifa 300
 QY 301 ETSDILORTVHVPSLPOAVLHVYIAHNTIAFLFAVVEQRTVTPKHQEVFECHPCV 360
 Db 301 etsdilhmvhlvhsllqgmthakylhnsyntactlfhellykqckllssngelllyegrrlv 360
 QY 361 LEPSLAONHTAASPRITLFSMSSDTPKGLAFRDALDPRKRVVDLQADYSTRAGV 420
 Db 361 lerpqlaghrfkcteenplfvstrepnlqilyle--kislrvhprydlidgasmakal 418
 QY 421 LGAGYQALMLARVLLDQALMLRGLHVLVLEVLQDPTCOOTL-----EVTPT 465
 Db 419 tgvvcyacrslalllygelmrkgirlvlelkkdynevhkktewvltldfclmrlekt 478
 QY 466 ALLVLGSSLGTERFSSSGMPDVERKEATELRTLOLTELSELKSGHNTETORSISCL 525
 Db 479 vkvy-----eklmkin--leaelgeladlthklrlrissgqtlsetlsqldidsrlspg 529
 QY 526 GE--ELTKNRDQIHEDNKSIOKICCDKMHFTYKQFKSRMPGSLSYNEQIHKLDKNV 583
 Db 530 gsladawehgeqcthpkrtneklqvlncmteilygkfkkaerrlayneeqihktdkqk 569
 QY 584 FSHLAKRLLOVFOECVQVTVSVLTGKRMROVORAKNHLHLSHVAACSEAGCAOE 643
 Db 590 lyhatakmtthfdecvkkyaeflnkeewlrmlhrlkqlldltnqcfdeevkkyge 649
 QY 644 SLNKIFPOLLDLR-ASRQGAEVSFQPMAPHPGDPKDLVFMQELCNMKLAFDLQDNN 702
 Db 650 ytnelgetlpqkmtfaassgikhtmtptlypsn--tlvemtlgmkklkeemegyvkealaenn 708
 QY 703 RLIER 707
 Db 709 hiler 713

RESULT 13
 AA07905
 ID AA07905 standard; Protein; 729 AA.

AC AA07905;
 DE 01-NOV-2001 (first entry)

XX Human inhibitory kappa B kinase 4 (IKK4).

XX Human: inhibitory kappa B kinase 4; IKK4; interleukin-8; IL-8;
 KW NF-kappa B; nuclear factor-kappa B; inflammation; allergy; asthma;
 KW atopic dermatitis; arthritis; rheumatoid arthritis; gout; SLE;
 KW systemic lupus erythematosus; glomerulonephritis; gene therapy;
 KW lipopolysaccharide-induced contact dermatitis.

OS Homo sapiens.

XX WO200144444-A2.
 PN
 XX 21-JUN-2001.
 PD
 XX 14-DEC-2000; 2000MO-JP08873.
 PF
 XX 14-DEC-1999; 99GB-0029542.
 PR
 XX (GLAX) GLAXO WELLCOME KK.
 PA
 XX Hashimoto Y, Takemoto Y, Furuta M, Sakai Y;
 PI WPI; 2001-398143/42.
 DR N-PSDB; AAD14494.
 XX
 XX Novel inhibitor kappa B kinase 4 protein which activates interleukin-8
 PT gene, and other inflammatory related genes, useful for identifying
 PT modulators of protein activity which are useful for treating arthritis,
 PT asthma
 PS
 XX Claim 1; Fig 8-9; 31pp; English.
 PS
 XX The present sequence is human inhibitory kappa B kinase 4 (IKK4).
 CC The IKK4 protein regulates interleukin-8 (IL-8) gene via the
 CC nuclear factor (NF)-kappa B site. The protein is useful for screening
 CC agents with antiinflammatory activity. Modulators of IKK4 is useful for
 CC treatment or prophylaxis of a disorder which is responsive to modulation
 CC of protein activity in a mammal. The IKK4 modulators are particularly
 CC useful for treating diseases involving inflammation and allergies such
 CC as asthma, atopic dermatitis, arthritis, rheumatoid arthritis, systemic
 CC lupus erythematosus, lipopolysaccharide-induced contact dermatitis,
 CC glomerulonephritis and gout. The IKK4 polynucleotide is useful for
 CC preparing probes which are utilized to screen a cDNA or genomic library.
 CC The antibodies against protein are useful for purifying protein or its
 CC portion and to locate the protein in tissue expressing the protein.
 CC Complementary or antisense strands of IKK4 polynucleotide is useful
 CC for gene therapy. The regulatory regions controlling expression of
 CC protein is used in gene therapy to control expression of the therapeutic
 CC construct in cells expressing IKK4 protein.
 CC
 XX Sequence 729 AA.
 SQ

Query Match 44.6%; Score 1660; DB 22; Length 729;
 Best Local Similarity 46.6%; Pred. No. 1.3e-140;
 Matches 338; Conservative 130; Mismatches 227; Indels 30; Gaps 7;

QY 1 MOSTNYLWHTDDLGAGATASYKARKKSGEVAVKVFNASYSRRPEVOYREFEVR 60
 DB 1 mgsushlw1sqdlqggtanvfrgrhkktdlfaikfnnsflrpdvqmfrefevik 60
 QY 61 RHNHONIVLEAVEETGSGROKVLMEVCSGSLVLEDPENTGTSFEETPLVYRCV 120
 DB 61 klmhkivlfaeectctrhkvlmetfcpgslvlecpnagylpseflivtrdv 120
 QY 121 AGNHLRENGIVHRDIPGNIMKLVGEESQSYIKLSDFGAARLDDERFVSYYGTEYL 180
 DB 121 ggmnhlrengivhrdipgnimkvgedqsvykldfgaarelededqfvsygyeql 180
 QY 181 HPMYERAVLRKFOAKAFGYTVDLMSIGYTLNHAATGSLPFLIPGGRPKNKELMTTTE 240
 DB 181 hpmeyeravlrkfdhkgkkyatvdlwslgylfynaagslpflrpfeggrnkemvylilig 240
 QY 241 KPGALISGQKOBNGPLEMSYSLPITCRLSMGLOQLVPLINILVEEDKCKGPFQOFA 300
 DB 241 kpgalisygkqkengpidsvgampvscslrgvlllpvlnilaedqekcwgtdqfa 300
 QY 301 ETSDLQRFVIVHSFPOAVLHHVYTHAHTIAIFLEAVEYEQNTVYRKQEVYLFEGHPCV 360
 DB 301 etadllhmrvlhwfslqgmahkylhysyntatlfihelvykqkllsnqellgyegrlv 360
 QY 361 LEPSLSAQHIAHTAASSPLTLFSMSDTRKGLAFRDPALDVRKFPVKDLQADYSTAKCV 420

DB 361 leprlaqhfptteempifvsvreplntlglye--kislphvprydlgdasamakl 418
 QY 421 IGAGYQALMLARVILDDGQALMIRGLHWLEVLQDPCQOTL-----EVTRT 465
 DB 419 lgvvcyacrllastlllygelmrkgilrwlleiklddynevtvkhkvevltldfcitnlekt 478
 QY 466 ALLYLGSSLGTFEFGSGMPDVERKATELRPLQTLSELSKSNHMETORSLSCL 525
 DB 479 vkvy-----eklnkin--leaaelgeistdhtkllllsssgtletsigd:asrlspg 529
 QY 526 GE-ELKRNDOIHBDNKSIOKIQOCLDKMFIYKQPKSRMRPGLSYNEQO:HKLDKVN 583
 DB 530 gladawahgegtbnpkdrnveklgylIncmteiygyfkfkaerriayneeq:lkfdkqk 589
 QY 584 FSLAKRLQVQRECVQYQVSLVTHGKRMRQVRAONHLHLGHSVATCSKARQOE 643
 DB 590 lyhatkmtchtdedcvkkyeaflnkseewlrmkhlrkqlslstngcdfdecevsxyqe 649
 QY 644 SLNKIFDQLLDR-ASEGCAEVSPPMAPHPQDPDKDLVFMHQLCNMKLLAFDLDNN 702
 DB 650 ynelgetlpqkmtfssagikhtmtipysn-tlventlgmkklkeemegvvelaenn 708
 QY 703 RLIER 707
 DB 709 hiler 713

RESULT 14
 AAB65601
 ID AAB65601 standard; Protein; 729 AA.
 XX
 AC AAB65601;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Novel protein kinase, SEQ ID NO: 126.
 XX
 KW Human; mouse; protein kinase; antiarthritis; antisclerotic; osteopathic;
 KW immunosuppressive; cardiant; renal; antiinflammatory; antistatic;
 KW dermatological; antidiabetic; antinfertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
 XX
 OS Homo sapiens.
 XX
 PM WO200073469-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000MO-US14842.
 XX
 PR 28-MAY-1999; 99US-0136503.
 XX
 PA (SUCE-) SUGEN INC.
 XX
 PI Plowman GP, Martinez R, Whyte D, Sudersanam S;
 DR WPI; 2001-032161/04.
 XX
 PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers -
 PS
 PS Claim 10; Fig 1; 310pp; English.
 PS
 CC The present sequence is a novel protein kinase. The novel protein kinases
 CC and the nucleic acids that encode them may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and

complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders.

Sequence 729 AA:

Query Match 44.6%; Score 1660; DB 22; Length 729;
Best Local Similarity 46.6%; Pred. No. 1.3e-140;
Matches 338; Conservative 130; Mismatches 227; Indels 30; Gaps 7;

QY 1 MOSTNTYMTDLDLGAGATASVYKARNKSGEVAVKVFNSASYRPREVOAREFEVLR 60
DB 1 mgstsnhlwllsdllggatanvfrgrhktgdlfaikvfnisflirpvdvqmrefevlk 60
QY 61 RINHOINVLEAVEETGSGROKVLIMEYSSGSLSVLEDPENTGSLSEEPVLYLRGV 120
DB 61 kinhnivklfaeeettirhkvlimetfcpslytlveepsnagylpeseellivrdyv 120
QY 121 AGMNHLRENGIYHARDIKPKNIRLWEGEGOSYKLSDDGAARLDDDKPVSVTEHYL 180
DB 121 gsmnhlrengiyhrdkipgnimrvlgdggyvklldfgaaealdedqfvslygleeY 180
QY 181 HPMTERAVLRKPOQKARCVTVLMSIGVTLVHAATGSLPIFPGPRNKEIMRYTTE 240
DB 181 hpmteravlrkqhkgkyatvdvlsigvtfhaatgslpifpgprnkeymkity 240
QY 241 KAGALISGQKQENPLEKSYSLPTCRLSKGLQNOVPLIANILFEEDKCKWGFQFA 300
DB 241 kpsgalisgqkaenplidsgmpvscslsglyqlcpvianlileadeqekwgfqfa 300
QY 301 EPSDILQRTIVHFSLPQAVLHNVYIHAHNTAIFLEAVYEGOTNTVPKHOEYLFEGHCY 360
DB 301 etsdilhmvnlhvfslqgmahkylhynctafihelvyqgklsnqelivegrtlv 360
QY 361 LEPSSAQHIAHTAASSPLTFSSMSDTPKGLAERPDALDVPKVPKVDLQADYSTAGV 420
DB 361 lepqlaghtfpkteempifvrsreplntiglye-kislpkhpnyrdldgdaamakal 418
QY 421 LGAGQALMLARVLLDGGALMRCGHVLEVLQDRCQTL-----EVRT 465
DB 419 tgvvyaactiacllllygelmhkgrtylelkdqdynevtvhtkevtltdfcirnekt 478
QY 466 ALLYLGSSLGTERFSSGSGMPDVORRKEATLRLQTLSELSKSHNVEFQSL 525
DB 479 vkvy-----eklnkin-leaaelgelsldhckllrlassqgfielsididarlspg 529
QY 526 GE-ELLNKRDQIHEDNKSIOKIQCCLDKMHFYKQFKSKMRPGLSYNEQOIKRLDKN 583
DB 530 gsladawahgegtbhpkdtrveklqyllnometeiygfkfkdkaerrlayneeqihfdkq 589
QY 584 FSHLAKRLLOYFQECVQTYQVSLVTHGRMROYORANHHLGHSAVATCNSERKAOE 643
DB 590 lyynatkamcthtdecvckkxkyaflnkseewlrkmhlirkgllstlnqcfdiieeskyge 649
QY 644 SLNKLIFDLDLDR-ASBEGAEVSPQPNAPHPGPKDLVFMQELCNMKILAFDLONN 702
DB 650 ylnelgelcpqkmftaassgikhtmplypsn-ltventlmkklkeemegvavelaenn 708
QY 703 RLIER 707
DB 709 hiler 713

RESULT 15
ID AAY80280
AA AAY80280 standard; Protein: 729 AA.

AC AAY80280;

DT 26-MAY-2000 (first entry)

DE Murine I kappa B kinase-related kinase 2 SEQ ID NO:4.

KW Mouse; murine; I kappa B kinase-related kinase; IKR-1; IKR-2;
KW protein kinase; immunomodulatory; antiinflammatory; antitumoridal;
KM cyostatic; autoimmune; inflammatory; infection; neoplastic disease.

OS Mus sp.

PN WC200008179-AL.

PD 17-FEB-2000.

PE 04-AUG-1999; 99WC-US1578.

PR 04-AUG-1998; 98US-0095269.

PR 11-SEP-1998; 98US-0099973.

PR 05-FEB-1999; 99US-0118783.

PA (IMM) IMMUNEX CORP.

PI Bird TA, Virca GD;

DR WPI: 2000-195583/17.

DR N-PSDB: AA295276.

PT Novel kappa B-kinase related kinases IKR-1 and IKR-2 used as molecular weight markers and in peptide fragmentation studies

PS Cialm 13; Fig 4; 85pp; English.

The present sequence represents murine I kappa B-kinase related kinase 2 (IKR-2). IKR proteins have immunomodulatory, antiinflammatory, antitumoridal and cyostatic activities. IKR polynucleotides can be used to express the proteins, and as probes to identify nucleic acids encoding proteins having kinase activity. IKR-1 and IKR-2 proteins and fragmented polypeptides are used for purifying proteins, e.g. to purify binding partner proteins; to measure protein activity, e.g. as quality assurance agents to monitor shelf life and stability of binding partner proteins. They may also be used as research agents, e.g. in assays to determine protein kinase activity, to identify novel molecules involved in signal transduction pathways, and to identify therapeutic compounds, to identify substances which interfere with the rate of substrate phosphorylation (such compounds would be useful for the treatment of autoimmune, inflammatory, infectious or neoplastic diseases), as molecular weight and isoelectric focusing markers, as controls for peptide fragmentation. Identification of unknown proteins, e.g. by comparison with proteins in databases and for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunospecificity chromatography. The antibodies can also be used to block binding of the IKR polypeptides to their binding partners.

Sequence 729 AA:

Query Match 44.2%; Score 1647; DB 21; Length 729;
Best Local Similarity 46.4%; Pred. No. 2e-139;
Matches 337; Conservative 129; Mismatches 228; Indels 32; Gaps 8;

QY 1 MOSTNTYMTDLDLGAGATASVYKARNKSGEVAVKVFNSASYRPREVOAREFEVLR 60
DB 1 mgstsnhlwllsdllggatanvfrgrhktgdlfaikvfnisflirpvdvqmrefevlk 60
QY 61 RINHOINVLEAVEETGSGROKVLIMEYSSGSLSVLEDPENTGSLSEEPVLYLRGV 120
DB 61 kinhnivklfaeeettirhkvlimetfcpslytlveepsnagylpeseellivrdyv 120

Db	61	klmhknuivklfaaleeecttrrhkvllimefcopcslylvcleepsnaugylpseffilivdrv	120
Qy	121	AGMHHLAENGTIVNDIDRPNIMLVEEGGSYTKLSDFGAARKLDDDEKRVSYTGEETL	180
Db	121	gsmhltlrenglvthdrlprnltmvldsgdsyvkltlffgaareldedegvslsygteeYl	180
Qy	181	HPDYERAVLJRKPOOKAFWTVVDLMSIGVILYHAATGSLPFIFFGSPRNKKEIMYRTTE	240
Db	181	hpmmyeraavrltkdqkkygatlwsygvclfyfmaagslprfgrfeprrtkemykylfig	240
Qy	241	KPACAGISGTOKEONGRPLEMSTSLPTCRSLSMGLQNDLVPILANILEVEEDKCKMGFDQFA	300
Db	241	kpsgaigsvqkaeongrpldswgdmplscslsqglqalltprylanllleadgskcwgfdfga	300
Qy	301	ETSIILORTVYHVFSLPQAVLHNHYIHANHTIAPLEAVYEGONVTMPKHOEYLFEGHPCV	360
Db	301	etsdvlhnmvhlvisldqmhanklylinsynlaaeafinelvykqtklvsngelilyegrrlv	360
Qy	361	LEPSLSAOHIAHTAASPRTLFSMSSDPTPKGLAFRDPALDPKRVKVDLQADYSTAKVY	420
Db	361	lelgrlqbfhpkctleempilfvtvsreqintvlglye--klsrlphpryalldgdaamakav	418
Qy	421	LGAGYQALMLARVLLDDQALMLRGLHNVLEVLDTCQQL-----EYTR	465
Db	419	tgvvcyaactstcllylqgelmrkvatvaveivkddayelvhkktlevvltldfctirmlekt	478
Qy	466	ALLYGSISLACTERESSSGMPDVOERKEATELRLTDLSEILSKCSHNTEFQRLSLCL	525
Db	479	vkvy-----eklmxvn--leaaelgejedisdkllrlsbsqglieslqldslsrslspg	529
Qy	526	G--BEELKANRQDIEHDNKSIOKIOCCSLDKMHNFTYKOFKSKSRMRPGSLSYNEQDILHKIDKVN	583
Db	530	glladtwahgeqthpridrnevklvlllncletaylqglfkkaertrlayneeqglltkdtkqk	589
Qy	584	FSHLAKRLLOYFOECVOTYOVSLVTJGSKRYROVORAOHNLHLIGHVATCNSEARGAOE	643
Db	580	lyynhatkmshtfseecyrktyeaftdkseemwtkmlhlrtkqlslstncqfdeevskyyqd	649
Qy	644	SLANKIFDQLLLDRASEQGAEVSPOPMAP--HPGRDP--KDLVFHMOELCSNDKLLAFDLQDN	701
Db	650	yltnelgetlpqkmlaaasg--vkhamaarypsnsltvmctgmklkleeamegvlvklaelaen	707
Qy	702	NRLTER 707	
Db	708	nhllter 713	

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 14, 2002, 19:11:28 ; Search time 67.53 Seconds

(without alignments)
259.339 Million cell updates/sec

Title: US-09-582-397A-4

Perfect score: 3726

Sequence: 1 MOSTTNTLMTDLGGGAT.....LQNNRLIERLHVPSPADV 717

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1660	44.6	729	1	US-08-971-937-2
2	1660	44.6	729	2	US-08-812-533-2
3	437.5	11.7	756	2	US-08-887-518-4
4	437.5	11.7	756	2	US-09-023-321-4
5	437.5	11.7	756	2	US-08-890-853-2
6	437.5	11.7	756	2	US-09-032-475-2
7	437.5	11.7	756	2	US-09-099-125A-2
8	437.5	11.7	756	2	US-09-099-125A-2
9	437.5	11.7	756	4	US-09-032-476-2
10	437.5	11.7	756	4	US-08-890-854-2
11	437.5	11.7	756	4	US-09-023-324-2
12	437.5	11.7	756	4	US-09-168-629-15
13	436.5	11.7	756	4	US-08-910-820-9
14	356.5	9.6	745	2	US-08-887-518-3
15	356.5	9.6	745	2	US-09-023-321-3
16	356.5	9.6	745	2	US-09-032-475-3
17	356.5	9.6	745	4	US-09-168-629-2
18	356.5	9.6	745	4	US-08-910-820-10
19	356.5	9.6	745	4	US-08-810-131A-2
20	352.5	9.5	745	2	US-08-890-853-4
21	352.5	9.5	745	2	US-09-099-125A-4
22	352.5	9.5	745	2	US-09-099-125A-4
23	352.5	9.5	745	4	US-09-032-476-4
24	352.5	9.5	745	4	US-08-890-854-4
25	352.5	9.5	745	4	US-09-023-324-4
26	337	9.0	584	3	US-09-160-483-1
27	299.5	8.0	582	4	US-09-428-711A-2

28	299.5	8.0	1051	4	US-09-428-711A-14	Sequence 14, Appl
29	294.5	7.9	1037	4	US-09-428-711A-21	Sequence 21, Appl
30	294.5	7.9	1050	4	US-09-428-711A-16	Sequence 16, Appl
31	287.5	7.7	1315	3	US-09-031-563-2	Sequence 2, Appl
32	287.5	7.7	1315	4	US-09-293-505-10	Sequence 10, Appl
33	285	7.6	454	2	US-09-159-385-1	Sequence 1, Appl
34	285	7.6	454	4	US-09-186-217-1	Sequence 1, Appl
35	284.5	7.6	1315	3	US-09-031-563-25	Sequence 25, Appl
36	283	7.6	648	3	US-09-031-563-5	Sequence 7, Appl
37	283	7.6	647	3	US-09-031-563-5	Sequence 5, Appl
38	279.5	7.5	260	3	US-09-031-563-24	Sequence 24, Appl
39	275	7.4	448	2	US-09-159-385-2	Sequence 2, Appl
40	275	7.4	448	4	US-09-186-217-2	Sequence 2, Appl
41	271	7.3	729	2	US-08-677-298-2	Sequence 2, Appl
42	266	7.1	270	2	US-08-852-743-5	Sequence 5, Appl
43	266	7.1	270	3	US-09-185-370-5	Sequence 5, Appl
44	265	7.1	201	3	US-09-124-476-2	Sequence 2, Appl
45	265	7.1	201	4	US-09-577-796A-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-08-971-937-2
; Sequence 2, Application US/08971937
; Patent No. 5776717
; GENERAL INFORMATION:
; APPLICANT: Cao, Zhaodan
; TITLE OF INVENTION: TRAF2-Associated Kinase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,937
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/812,533
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-002
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-971-937-2

Query Match 44.6%; Score 1660; DB 1; Length 729;
Best Local Similarity 46.6%; Pred. No. 3, 2e-140;
Matches 338; Conservative 130; Mismatches 227; Indels 30; Gaps 7;
OY 1 MOSTTNTLMTDLGGGATASVYKANKKSGEVAVKVNASVYRPPVGVREFEVLK 60
DB 1 MOSTTNTLMTDLGGGATAVNFGRHKKTKYGDIFAIVKVNNTSFLRPVGVYQKREFEVLK 60
```

[illegible]

RESULT 3
US-08-887-518-4
Sequence 4, Application US/08887518
Patent No. 5843721
GENERAL INFORMATION:
APPLICANT: Roche, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-887-518-4

Query Match 11.7%; Score 437.5; DB 2; Length 756;
Best Local Similarity 23.5%; Pred. No. 1.5e-30;
Matches 187; Conservative 118; Mismatches 308; Indels 183; Gaps 27;

QY 9 WHRDDLLGGATATATYKARKKSGEYVAAYKVENASATYRRPREYQVREFEYLRLHONIV 68
DB 15 WKKERLGTGCGFNGVIRHMQETGEQIAIKOCROELSPRRRERMCLEIIMRLTTHPNV 74
QY 69 KLFAYEE---TGSRQKVLIMEYCGSSGLSVLEDPENTFGLESEPEFLVLRCAVAGN 124
DB 75 AADVVEGKONLAPNDPLILAMETCOGGDLKRLNPFENCCGIRBAILTLISDIALR 134
QY 125 HLRENGIVHRDIKPGNIMRLVGEESGYIKLSDFGARKLIDDEKFEVSYGTEEYLAPDM 184
DB 135 YLHENRIIHRDLKPNIVLQGGEO-RLIHKIIDLAGAKELDQSLCTSPFGTLYLAPEL 193
QY 185 YERAVLRKPOQKAFGYTVVLMSTGVLVHAATGSLPFIPEGCP-----RRKELMYRI 237
DB 194 LE-----QOKYTVTVVDMWMSGTLAFECITGFRPFLPMQOVOMHSHVROKSEVDIV 245
QY 238 TTEKPAIGATSGTQKENGPLEYSYSLPTICRLSMGLONOLVPLIANIL-----EVEDK 292
DB 246 SEGL-----NGYKFESSSLPYRNINLSVLAERLEKKLQMLMMHPQGTDP 293
QY 293 WGDQCPAETSDILORTVIVHESLPQAVLHNVY IHAHNTAIFLEAVYEQTNVTPRHOEY 352
DB 294 YGNGCGFKALDDITLKLIVILNMVTGIHTYVTEDESQSLKARIQODTGIPEDQEL 353
QY 353 LPEGHCPVLEPSLSAQHIA-----HTAASSPLTIFSMSSDTPKGLARDPALDVPKYV 405

DB 354 LOEAGIALIPDKPATQCSIDGKLNIGHTLMDVLVLFDSNKITYETQISPRPQ---PESV 410
QY 406 -----PKVDLADYSTAGVAGAGVQALMLARVLDDGALMLRLHM-VLEVLDPTQOQ 458
DB 411 SCILDEPKRNL-AFQOLR-----VW-----GQVHSTQTLKEDCNR 446
QY 459 TLEVTRTALLYL-----GSSIGTERFSSGMPV----- 488
DB 447 LQGGRAAMNMLLRNNSCSTKKNMAMSMQDLKAKLDEFKTSIQIDLEKYSIDQTEGIT 506
QY 489 -----QERKEATEL---RTRLOTLSEILSKSHNVTQRS-----LSCLGEE 528
DB 507 SDKLLAMREMQAVEALCGRENEVKILVERMMALQTDIVDQDRSPMRKOGCTLDLDEQ 566
QY 529 LL-----KNRDOIHEDNKS-----TOKTQCCLDKHFITYKQFKSRMRPGSTYNEE 574
DB 567 ARELIRRLREKFRDQTEBDSQEMVRLQLQAIQSEKRVRYITQIST-----VVCOK 621
QY 575 QIHKLKDVNFSLAKRLLOVPOECVQTVQVSLVTHGRK--NRQVQRAQNL-HLIGHSV 631
DB 622 ALELLPKV-----EV-----VSLMNEDEKTVRLQEKQKELMNLKTIAC 662
QY 632 ATCNSEARKAQESLKNITFQDLLDRASEGAEVSPQMA-----PIPGDPKDLVFHMOEL 687
DB 663 SKVRGPVSGSPDSMN-----ASRLSQGQLMSQPSSTASNSLPPAPAKKSEELVAEHNIL 715
QY 688 CNDMKLLAFDLDONNR 703
DB 716 CT---LLENATDITVR 728

RESULT 4
US-09-023-321-4
Sequence 4, Application US/09023321
Patent No. 5844073
GENERAL INFORMATION:
APPLICANT: Roche, Mike
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/887,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-023-321-4

Query Match	11.7%;	Score 437.5;	DB 2;	Length 756;
Best Local Similarity	23.5%;	Pred. No. 1.5e-30;		
Matches 187;	Conservative 118;	Mismatches 308;	Indels 183;	Gaps 27;

QY	9	WHTDOLLQGGTAAVYUAKRNKSGEVAUVAFNSASYRPREYQVREFEVRLRNHONIV	68
Db	15	WEMERLSTGGFGVNIKNHNOETEOJAIKOCROELSPRNERKCLTEIQIMRRITHPNV	74
QY	69	KLFAVEE---TGSSROKVLIMEXCSSGSLSYLEDEPNTFGISEEFVLVLRVAGMN	124
Db	75	AARVPREGMVLAPNDPRLPLAMEXCOGGDLRKYLNQENCCGLREGAILFLDLSASLR	134
QY	125	HLRENGIYHRIKGNIMRLVGECSOTYKLSDFGAARKLDDDEKFSVYGTETYLHPDM	184
Db	135	YLHENRIIHRKLEKENTVLOOGEQ-RLIHKIDIGVKEKEDOGSLCSFGOTLOYLAPEL	193
QY	185	YERAVLRKPOOKAGVYVWDSIVTSVTLHYATAGSLPIRPGGP-----RNKKEIYRI	237
Db	194	LE-----OQKTVYVDVMSPECTLAFECTIGRPLPMOPROMHASKRQASEVDIV	245
QY	238	TTKRPAGISGTQOENGPLEWMSYSLPTCRKLSMGIONQVPILANIL-----EVEDKC	292
Db	246	SEDL-----NGTVKFSSSLPYPNMLNSVLERLEKVLQIMLMHNPGRGDP	293
QY	293	WGFQGFAPETSDIIQRYVHVFSLPQAVLHHVYIHAINTAIFLEAVYEDQNTYPRKQET	352
Db	294	YRPGCFEADDDIINLKVLHILNVGTITHYPTEDESLOSLKARIQDPTGIPREDOEL	353
QY	353	LFEHGPCVLEPSSLAONHIA-----HTAASSPLTFESMSDPRKGLAFDPALDVPKFV	405
Db	354	LQELGALIPKPRPTQCSODSKLMEGHTLDMDLVFLFDNSKITIETQISPRPQ---PESV	410
QY	406	-----PKVDLOADYSTAKGVLYGAGYALMLARVLLDQALMLGLHW-VLEVLODTCQO	458
Db	411	SCILOEPRRL-AFFOLRK-----VW-----GQVHHSIQTLKEDCNR	446
QY	459	TLEVTRALLVLT---GSSLIGHERSSGGMV-----	488
Db	447	LQGGORAMMMLLNNNSCLSKKXKSMASMSOOLAKLIDFKTSLQIDLEKYSDEQTEGIT	506
QY	489	-----OERKEATEL---RTIRLOTLSELKSCSHNVTEFORS-----LSCIGE	528
Db	507	SDKLLAMREMEQAVELCGRENEVKLLVERMMALQOTIVLOQSRPMKROKGGTLDLEEQ	566
QY	529	LL-----KNRQIHEDNKS-----IQKIOCCDKMHFTYKQFKKSMRPGSLSYNEE	574
Db	567	ARELYRLREKPRDORTGEGSQEAMVRLLOALOSFEKKVAVITYOLSKT-----VWCOK	621
QY	575	QIHKLIDKVFNSHLAKRLLQVQEECVQYQVLSLTVHCKR--MRQYQAOQHIL-HLIGHSV	631
Db	622	ALELLPKV-----EEV-----VSLMNEDEKTVLRLOERKQKELNMMLKTIAC	662
QY	632	ATCNSSEARGAESLNTKIFDOLLDRASEQAEVSPQMA-----PHPRDPDKDLVFIHQEL	687
Db	663	SKVGPVSGSPDSKN-----ASRLSQPQGLMSQPSPTAASNLSPRAKKSEELVAEHNIL	715
QY	688	CNDKLLAFDLOQDNRR	703
Db	716	CT---LLENALIODTVR	728

RESULT 5
 US-08-890-853-2
 : Sequence 2, Application US/08890853
 : Patent No. 5851812
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Goeddel, David V.
 : APPLICANT: Woronicz, John
 : TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 : NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
600 BAY STREET SUITE 2000

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: E] 0001

MEDIUM LIFE: FLOPPY
COMPUTER: TRW 600

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Rel

CURRENT APPLICATION DATA:

APPLICATION

FITTING DATE: _____

CLASSIFICATION: A35

400
 CIRCULATION.
 INFORMATION

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,62

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION

TELEPHONE: (415) 343-4344

TELEFAX: (415) 343-4344

NEOPHANTON FOR ECO ID NO: 040 404

STATION FOR SEX I
NE ORALION FOR SEX I

SEQUENCE CHARACTERISTICS

LENGTH: 756 amino acids

TYPE: amino acid

STRANDED]

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;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      MS-09-000-053-3

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Query Match      11.7%; Score 437.5; DB 2; Length 756;
Best Local Similarity 23.5%; Pred. No. 1.5e-30;
Matches 187; Conservative 118; Mismatches 308; Indels 183; Gaps 27;

OY      9 WHTDDLCOGATASYKARKNKSGEVAVKVFNSASYPRPPEVOYREEFVLRRLNHNIV 68
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      15 WEMKRLCTGCGFNGVNIIRHNNQETGQIAIKOCROELSPRNERBWLCTEIQIMRLTHPVV 74
OY      69 KLFAYEE-----TGGRQKVLIMECYSSSSLLSVLEDPENTGSLSEEFVLVRCVAAQM 124
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      75 AARDYPEGMNLAPRDPDLPLAMEYIQGGDLRKRYLQWFENCCGLRGAILTLTSLDASALR 134
OY      125 HLRENGIVHRDIKPGNIMRLVGEEOGSITKLSDFGAARKLDDDEKFAVSVGTGEYLHADM 184
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      135 YLHERIRIHRDLKPENIVLQOGEQ-RLIKHITIDGAKELDQGSCTSFVGIIQYLADEL 193
OY      185 YERAVLRKRPQKAKFENVTDWLSIGVTLVHANTGSLPFIFFGPR-----RRNKIMRI 237
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      194 LE-----OQKYVIVDVWSFGFLAECTIGGFPRPLPRNQPVOMHRSVKRQSSVDIV 245
OY      238 TTEKPAGISGTOKEENGPLEMSYSLLPTFCRLSMIGLQOLVILANIL-----EVEEDKC 292
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      246 SEDL-----NCTVFKSSSLPRPNNINSLVARLEKWKIQLMIMHPRQGTPT 293
OY      293 WGFDOFPEFETSDIILQRIYIHVFSLPQAVLHVHYIHAHTIAIFLEAYVEQTNVPRKHOEY 352
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      294 YGPNCFCFALDDILNLTAKLVILIMVTGTHIHYPTVEDESLQSLKARIOQDTGIDPEEDQL 353
OY      353 LFEHGHPCLVLEPSLSAQHIA-----HFAASSPLTFEMSSDTPRGLAFFRPALDVPRFY 405
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      354 LOEAGLALIPKPAOCISDGKLNKGHLLMDLVFLFENSKIITYETQISPRPQ--PESV 410
OY      406 -----PKVDLOADYSTAKVIGAGYQALMLARVLDDQALMLKRLAH-VLEVLDDTQQ 458
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      411 SCLIOEPRRLN-AFFQLRK-----VW-----GQVHNSIQTLEKDCNR 446
OY      459 TLEVYRTALLYL---GSSLGTERFSSGSGMPDV----- 488
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      447 LQOQGRAMMILIRNNSCLSKKNSMSMSOOLKAKLIDFFFTSIOIDLEKYSQEQEFIT 506

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OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099,125A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/890,853
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-006-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 756 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-099-125A-2

Query Match 11.7%; Score 437.5; DB 2; Length 756;
 Best Local Similarity 23.5%; Pred. No. 1.5e-30;
 Matches 187; Conservative 118; Mismatches 308; Indels 183; Gaps 27;

QY 9 WHTDDLGGATASVYKANKKSGEVAVVAFNSASVRRPPEVQVREPEVRLNHOIV 68
 DB 15 WEKMERLGTGGGVNIRHINDETGEQIAIKOCROELSPRNERKWCLEQIMRRLTHPVV 74
 QY 69 KLFAYE-----TGGRQAVLIMEYSSGSLSVLEDPENTGLSEEFVYLRCVAGMN 124
 DB 75 AARDPEGMQNLAPNDLPLAMEYCOGDLRKYLNOFENCCGLREGALITLLSDIASALR 134
 QY 125 HURENGIYHDIKPGNINIRLVGEGOSIYKLSDFGAARKLDDDEKFPVSVTEEYLPDM 184
 DB 135 YLHEKRIITHRDLKPNVYLQOGEQ-RLIHKTIIDLGAYAKELDQGSICSPFTTQYLAPEL 193
 QY 185 YERAVLRKPKQKATGVVDVLSIGVTLVYHATGSLPFIFGSP-----RRNKEIYRI 237
 DB 194 LE-----QOKTVVDVMSFGTIAFECITLTPRPPLPNQOPQMSKRYKQKEVIVV 245
 QY 238 TTEKPAKALISTOKOENPLFMSISLPITCRLSMGLQNLVPLIANIL-----EVEDKC 292
 DB 246 SEDL-----NGTVKFSSSLPYPNNLNSVLAERLEKWLQMLMHPRGRTDPT 293
 QY 293 WGFQOFPAETSDILQRYIVHVESLQAVLHHVYIHAHTIAIFLEAVYEQTNTVPKHOEY 352
 DB 294 YGRPGCFRALDDIILNKLIVHLINVTGTIHYVPTEDESLOSUKARIQODTGIPREDOEL 353
 QY 353 LFESHPCVLEPSLSAOHIA-----HTAASSPPLTFSSMSDPRKGLAFRDPALDVPEV 405
 DB 354 LQFAGLALIPDKPATQCSIDQKINEGHTLMDLVFLPDNKITYEPIISRPQ---PEV 410
 QY 406 -----PKYDQADYSTAKGVLAGGYQALMLARVLDDGALMRLGLHW-VLEVLQDTQQ 458
 DB 411 SCIIQEKRRNL-AFFQLRK-----VW-----GQVHISIQTLKEDCNR 446
 QY 459 TLEVTRTALVYL--GSSLTERFSSGSGMPDV----- 488
 DB 447 LQOGQRAAMNMLNNNSCLSKMNSMASMOQLKAKIDFKFTSIQIDLEKYSQOTERTGIT 506
 QY 489 -----QERKEATEL---RTLQVLSSEILSKCSHNVETORS-----LSCIGEE 528
 DB 507 SDKLLAMREMEQAVELGRENVEYKLLVERMMALQDTIVDLSRPGKRGCGGLDDLEQ 566
 QY 529 LL-----KNRQIHEDKMS-----IQKIOCCLDKMHFIYKQKRSKMRGSLYNEE 574
 DB 567 ARELYRLRKPRDQRTSGEQENVRLLQAIQSFEKRYVIVYTQIST-----VYCKOK 621

QY 575 QIHKLDKYNFSLAKRLLQVPECEVQTYQVSLYTHGR--MRQVQRAQNL-HLIGHV 631
 DB 622 ALLELPKV-----EEV-----VSLMNEDEKTVIRLOEKROKELNLLKTIAC 662
 QY 632 ATCNSEARGAQSINKIFDQLLDLRASEQGAESVQPM-----PHPGPDKDLVFHMQEL 667
 DB 663 SKVRGPVSGSPDSMN-----ASRLSQPGQLMSQPSSTANSLEPPAKKSEELVAYEAHNL 715
 QY 688 CNDKILAFDLQDNNR 703
 DB 716 CT---LLENALQDTVR 728

RESULT 8
 US-09-099-124A-2
 Sequence 2, Application US/09099124A
 Patent No. 5939302
 GENERAL INFORMATION:
 APPLICANT: Goeddel, David V.
 APPLICANT: Moronitz, John
 TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/099,124A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/890,853
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-006-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 756 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-099-124A-2

Query Match 11.7%; Score 437.5; DB 2; Length 756;
 Best Local Similarity 23.5%; Pred. No. 1.5e-30;
 Matches 187; Conservative 118; Mismatches 308; Indels 183; Gaps 27;

QY 9 WHTDDLGGATASVYKANKKSGEVAVVAFNSASVRRPPEVQVREPEVRLNHOIV 68
 DB 15 WEKMERLGTGGGVNIRHINDETGEQIAIKOCROELSPRNERKWCLEQIMRRLTHPVV 74
 QY 69 KLFAYE-----TGGRQAVLIMEYSSGSLSVLEDPENTGLSEEFVYLRCVAGMN 124
 DB 75 AARDPEGMQNLAPNDLPLAMEYCOGDLRKYLNOFENCCGLREGALITLLSDIASALR 134
 QY 125 HURENGIYHDIKPGNINIRLVGEGOSIYKLSDFGAARKLDDDEKFPVSVTEEYLPDM 184

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Db 135 YLHNRNIIHRDLKPNIVLQOGEQ-RLIHKIIDLGAKELDQSLCTSPVGTLOYLAPEL 193
OY 185 YERAVLRKPOOKAAGVTVLMSIGVTLVHAANGSLPEIPFGP-----RRNKELMYRI 237
Db 194 LE-----QOKYTVTVYWSFGTLAFECITFRFPFLPMQVONHSHKVRQKSEVDIV 245
OY 238 TTTPKPAIGASITGOKENGPLEMSYSLPTICRLSMGLONOLVPLIANIL-----EVEDK 292
Db 246 SEDL-----NGYKFFSSSLPYRNHNSVLAERLEKQLQMLMHPROGTDPT 293
OY 293 WGFDOFFAETSDILORTVIVHESLPOAVLHVYIHAHNTAIFLEAVYEDONTVPKHQY 352
Db 294 YGPNCGFKALDIDLNLKLVHILMVTGTHITVTEDESLQSLKARIQDPTGPREDQEL 353
OY 353 LFEHGPCVLEPSSLASOHA-----HTAASSPLTFLSMSSDTPKGLAFRDPALDVPKFV 405
Db 354 LQENGLALIDPKPATQICISGKLINEGHTLDMDLVFLFDSNKITYETQISPRPO---PEY 410
OY 406 -----PKYDLOADYSTAKGVLAGYQALMLARVLLDQALMLRGLHW-VLEVLADPTCOQ 458
Db 411 SCILQEPKRL-AFQOLR-----VW-----GQVHISIQTLKEDCNR 446
OY 459 TLEVTFRALLYL---GSSIGTERFSSSGMPDY-----488
Db 447 LQGGQRAAMNLLRNNSCLSKRMNSMAMSQOLKAKLDFEFTSIQIDLEKYSQTEFGIT 506
OY 489 -----QERKATEL---RTRLOTLSLSCSHNVETORS-----LSCIGEE 528
Db 507 SDKLLAMREMOAVELECGENEKLLVERMMALQTDIVDQSPMRKOGGTLDDLEQ 566
OY 529 LL-----KRDQIHEDNKS-----LOKIOCCDKMHFIYKQFKSRMRGSLSYNE 574
Db 567 ARELYRLRKPQDQTEGDSQEMVRLLLQAIQSFEKKVAVITYOLSKT-----VYCKOK 621
OY 575 QIHKLDKVNESHAKRLQVFOECVQYQVSLVTHGKR--MRQVQRAQNHU-HLIGHSV 631
Db 622 ALLELPKV-----EEV-----VSLMNEDEKTVVLAERLEKQLQMLMHPROGTDPT 662
OY 632 ATCNSEARQOESLNKIFDOLLDRASEGAEVSPQMA-----PHGPPDKDLVFHMOEL 687
Db 663 SKYRGVPSGSPDSMN-----ASRLSQPQOLMSQPSAHSNLPRAKKSEELVAAEHNL 715
OY 688 CNDKLLAFDLDNNR 703
Db 716 CT---LLENAIODTVR 728

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RESULT 9
US-09-032-476-2
; Sequence 2, Application US/09032476
; Patent No. 6235492
; GENERAL INFORMATION:
; APPLICANT: Roche, Mike
; APPLICANT: Cao, Zhaoan
; APPLICANT: R. gnier, Catherine
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,476
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/890,854
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: T97-006-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-032-476-2

Query Match 11.7%; Score 437.5; DB 4; Length 756;
Best Local Similarity 23.5%; Pred No. 1.5e-30;
Matches 187; Conservative 118; Mismatches 308; Indels 183; Gaps 27;

OY 9 WHTDILLGOGATAVYKARKKSGEVAAVKNFNSASRRPPEVQVREFEVLRNLNQNIV 68
Db 15 WEKKEKRLTGFGFQVYIRHINQETGEQIALKOCQELSPNRBRWCLEIQIMRLTHPNV 74
OY 69 KLFAYE-----TGGSRQKYLMEYCGSSGLSLVDEPENTFGISEEFLVYLKVVAGNN 124
Db 75 AARDVEGQONLAPNDLPLAMEYCOGDLRYLNOFENCCGIREGAILTLLSDIASALR 134
OY 125 HLENGIVHRDIKPGIMRLVGEESYKLSDFGAARKLDDEKRVSYGTEELHPDM 184
Db 135 YLHNRNIIHRDLKPNIVLQOGEQ-RLIHKIIDLGAKELDQSLCTSPVGTLOYLAPEL 193
OY 185 YERAVLRKPOOKAAGVTVLMSIGVTLVHAANGSLPEIPFGP-----RRNKELMYRI 237
Db 194 LE-----QOKYTVTVYWSFGTLAFECITFRFPFLPMQVONHSHKVRQKSEVDIV 245
OY 238 TTTPKPAIGASITGOKENGPLEMSYSLPTICRLSMGLONOLVPLIANIL-----EVEDK 292
Db 246 SEDL-----NGYKFFSSSLPYRNHNSVLAERLEKQLQMLMHPROGTDPT 293
OY 293 WGFDOFFAETSDILORTVIVHESLPOAVLHVYIHAHNTAIFLEAVYEDONTVPKHQY 352
Db 294 YGPNCGFKALDIDLNLKLVHILMVTGTHITVTEDESLQSLKARIQDPTGPREDQEL 353
OY 353 LFEHGPCVLEPSSLASOHA-----HTAASSPLTFLSMSSDTPKGLAFRDPALDVPKFV 405
Db 354 LQENGLALIDPKPATQICISGKLINEGHTLDMDLVFLFDSNKITYETQISPRPO---PEY 410
OY 406 -----PKYDLOADYSTAKGVLAGYQALMLARVLLDQALMLRGLHW-VLEVLADPTCOQ 458
Db 411 SCILQEPKRL-AFQOLR-----VW-----GQVHISIQTLKEDCNR 446
OY 459 TLEVTFRALLYL---GSSIGTERFSSSGMPDY-----488
Db 447 LQGGQRAAMNLLRNNSCLSKRMNSMAMSQOLKAKLDFEFTSIQIDLEKYSQTEFGIT 506
OY 489 -----QERKATEL---RTRLOTLSLSCSHNVETORS-----LSCIGEE 528
Db 507 SDKLLAMREMOAVELECGENEKLLVERMMALQTDIVDQSPMRKOGGTLDDLEQ 566
OY 529 LL-----KRDQIHEDNKS-----LOKIOCCDKMHFIYKQFKSRMRGSLSYNE 574
Db 567 ARELYRLRKPQDQTEGDSQEMVRLLLQAIQSFEKKVAVITYOLSKT-----VYCKOK 621
OY 575 QIHKLDKVNESHAKRLQVFOECVQYQVSLVTHGKR--MRQVQRAQNHU-HLIGHSV 631
Db 622 ALLELPKV-----EEV-----VSLMNEDEKTVVLAERLEKQLQMLMHPROGTDPT 662
OY 632 ATCNSEARQOESLNKIFDOLLDRASEGAEVSPQMA-----PHGPPDKDLVFHMOEL 687

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Db 663 SKVRGVSQSPDSMN-----ASRLSQPOLMSQSPSTASNSLPEPAKKESEELVAEAHNL 715
 QY 688 CNDMKILAFDLDNNR 703
 Db 716 CT---LLENALIDTVR 728

RESULT 10
 US-08-890-854-2
 ; Sequence 2, Application US/08890854
 ; Patent No. 6235512
 ; GENERAL INFORMATION:
 ; APPLICANT: Rothe, Mike
 ; APPLICANT: Cao, Zhaoan
 ; APPLICANT: R. gnier, Catherine
 ; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/890,854
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: T97-006-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 756 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-890-854-2

Query Match 11.7%; Score 437.5; DB 4; Length 756;
 Best Local Similarity 23.5%; Pred. No. 1.5e-30;
 Matches 187; Conservative 118; Mismatches 308; Indels 183; Gaps 27;

QY 9 WITDDLGGATASYKRNKSGEVAVKFNNSAYRRPEYQVREEVLRNLHNOIV 68
 Db 15 WEMKRLTGGGNGVIRKHNWDETGQIAIKOCROELSPRNRRCLETOIKRRLTHPVV 74
 QY 69 KLFVAVE---TGGSROKVLIMETSSGSLSLVLEDPENTFGLSPEEFLVLRGVVGMN 124
 Db 75 AARDVPEGMQNLAPNDLPLAMEYQGGDLKRYLNQFENCGGLGEGALLTLISDIASLR 134
 QY 125 HIRENGIYHRDIKPNIRLVLGEGOSIYKLSDFGAARKLDDDEKFEVSVYGTETYLHPDM 184
 Db 135 YLHENRIIHRDLKPNENIYLOQGEQ-RLIHKTIIDLGAKELDQGLCTSFVGTLLQYLAPEL 193
 QY 185 YERAVLRPOQKAFGVTVDMISIGTILHAATGSLPTFPEGP-----RRNKEMTRI 237
 Db 194 LE-----QOKYTVTVDMISFGLAECTGERPFLPNQPVQWMSKROKSEVDIV 245
 QY 238 TTEKPAIGASTOKOENPLSEMSYSLPTCRLSMGLQNLVPLANIL-----EVEEDKC 292

Db 246 SEDL-----NCTVKSSSLPYNNLNSVLAERLEKMLQMLMHPROGTDPT 293
 QY 293 WGFDOFFAFESDIIQRTVYHFSLPQAVLHVYTHANTIAIFLEANYEOTNTVTPKOEY 352
 Db 294 YGPNGCFEALDDIILNKLIVHTLNMVGTITHTYPTADESLQSLKARKIQDQDGLPEEDQL 353
 QY 353 LFEGHPCVLEPESLSAQHIA-----HTAASSPPLTFSSMSDFPKGLAFDPALDVKKFY 405
 Db 354 LQFAGLALIPKPAFQCSQDKLNEGHTLDMDLVFLFDNKSRTYETQISRPQ---PEVY 410
 QY 406 -----PRVIDIADYSTAKGYLGAGYQALMARVLLDQALMLGLHW-VLEVLDQTCQ 458
 Db 411 SCIIQEPKRNLAFFOLK-----VW-----GQVWHSIQTLKEDCNR 446
 QY 459 TLEVETRALVY---GSSIGTERFSSGGMVDY----- 488
 Db 447 LQCGORAMMMLLNNSCLSKMNSMASQOOLAKIDPFKTSIQIDLEKYSQTERGIT 506
 QY 489 -----QERKEATEL---RTRLOTLEILSKSHNVEFORS-----LSCIGEE 528
 Db 507 SDKLLAMREMEQAVELQGRENEVKLLVERMMAIQTDIVDQSPMKRKGGLDLEQ 566
 QY 529 LL-----KNRQIHEDNKS-----IQKIQCLDKMHFTYKQFKSRMRGLSYNEE 574
 Db 567 ARELYRLREKPRDQRTGDSQEWYRLLQALISFEKKVYIYQLSKT-----VYCKOK 621
 QY 575 QIHKLKVNFSHLAKRLQVQEECVQTYOYSLVTHGR--MQOVQAOHNL-HILGHSV 631
 Db 622 ALLELPKY-----EEV-----VSLMNEDEKTVVRQERKQELNWLKTIAC 662
 QY 632 ATCNSEARGAESLNTKIFDOLLDRASEGAEVSPQMA---PHRGPDKDLVFHMOEL 687
 Db 663 SKVRGVSQSPDSMN-----ASRLSQPOLMSQSPSTASNSLPEPAKKESEELVAEAHNL 715
 QY 688 CNDMKILAFDLDNNR 703
 Db 716 CT---LLENALIDTVR 728

RESULT 11
 US-09-023-324-2
 ; Sequence 2, Application US/09023324
 ; Patent No. 6235513
 ; GENERAL INFORMATION:
 ; APPLICANT: Rothe, Mike
 ; APPLICANT: Cao, Zhaoan
 ; APPLICANT: R. gnier, Catherine
 ; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 BUSH STREET, SUITE 3200
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,324
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/890,854
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: T97-006-1
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 756 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-023-324-2

Query Match 11.7%; Score 437.5; DB 4; Length 756;
 Best Local Similarity 23.5%; Pred. No. 1.5e-30;
 Matches 187; Conservative 118; Mismatches 308; Indels 183; Gaps 27;

9 WHTDLLGGAGATASYKARKKSGEYVAVKFNASAYRRPPEVQVREFEVLRNLHNIY 68
 15 WEKKEKLTGCGFNGVIRHNOETGEIOAIKOCROELSPNRREWCLEIQIMRLTHPNV 74
 69 KLFAYEE---TGSROKVLIMEYSSGSLSLVLEDPENTFGLSEEFVLVLCVYAGMN 124
 75 AARDVPEGMONTLPNDLPFLAMEYCGGDLRKYLNOFENCGLREGAILTLSDIASALR 134
 125 HLRNGIVHRDIKPGNIMLVGEEGSIYKLSDFGAARKLDDKVFVSYGTEYLHPDM 184
 135 YLHNRNIHRDLKPNIVLQOGEQ-RLIHKIIDLGAKELDQGSICTSFVGTIQYLAPEL 193
 185 YERAVLRKPOQKAFVTVDMISGVTLYHAATGSLPFIPEGP-----RRNKEIMYRI 237
 194 LE-----QOKYTVTVDMISGVTLYHAATGSLPFIPEGP-----RRNKEIMYRI 245
 238 TTEKPAIGASITGOKONGLEMSYSLPTCRLSMGLQNOVLPIANIL-----EVEEDKC 292
 246 SEDL-----NGTVKFSSSLPTYPNNLNSVLAERLEKWLQMLMWHPRQGTPT 293
 293 WGFDOFAETSDILOTVIHVESLPQAVLHNYIHANHTIAFLVAVYEOTNTPRKHOEY 352
 294 YGNGCGFKALDDILNKLIVHILMTGTIHTYPTEDSLSQAKARIQDDTGIPREDELT 353
 353 LFEGRHCVLPELSAOHIA-----HTAASPFLTFSSSDTPRGKLAFRDPAIDVPRV 405
 354 LQAGLALIPDKPATQICISGKLNIGHTLDMDLVFLFNSKITTEYQISPRQ---PESV 410
 406 -----PKVDLQADYSTAGVLAGYQALMLARVLLDQALMLGLHW-VLEVLODPTCOQ 458
 411 SCILDEPKRNL-AFQOLRK-----VW-----GQVHNSIQTLKEDCNR 446
 459 TLEVTRTALLYL-----GSSIGTERFSSSGMPDV----- 488
 447 LQOGQRAAMNMLLRNNSCKSKMNSMASWSQOLKAKLDFEFTSIQIDLEKYSQTEFGIT 506
 489 -----QERKEATEL---RTRIQTLSEILSKSHNVTETORS-----LSCIGEE 528
 507 SDKLLAMREMEQAVELCGRENEVKLLVERMALQTDIVDLORSPPGRKOGGTLDDLEQ 566
 529 LL-----KNRDOIHEDNKS-----IQKIQCCLDKMHFITYQOKFSRRMRFGLSYNEE 574
 567 ARELYRRLREKPRDQTEBDSQEMVRLILQAIQSFEKKVRYIYTOLSKT-----VVCOK 621
 575 QIHKLKDVNFSLAKRLLOVFOECVQYQVSLVYTGKR--NRQVRAQANHL-HLIGHV 631
 622 ALELLERKLV-----EEV-----VSLMNEDEKTVYRLQEKRKELMNLKIC 662
 632 ATCNSEARGAQLINKIPDOLLDRASEQAGAEVSPQMA-----PHGPRPKDVLVFMQEL 687
 663 SKYRGVSSPSDSMN-----ASRLSQGQLMSQSPSTASNSLPEAKKSEELVAFANHL 715
 688 CNDKMLAFDLDNNR 703
 716 CT---LLENALIDPTVR 728

RESULT 12
 US-09-168-629-15
 ; Sequence 15, Application us/09168629
 ; Patent No. 6242253

GENERAL INFORMATION:
 ; APPLICANT: Karin, Michael
 ; APPLICANT: Didonato, Joseph A.
 ; APPLICANT: Rothwarf, David M.
 ; APPLICANT: Hayakawa, Makio
 ; APPLICANT: Zandi, Abraham
 ; TITLE OF INVENTION: IKK Kinase, Subunits Thereof, and Methods of Using Same
 ; FILE REFERENCE: P-0D 3295
 ; CURRENT APPLICATION NUMBER: US/09/168,629
 ; EARLIER FILING DATE: 1998-10-08
 ; EARLIER APPLICATION NUMBER: 60/061,470
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 756
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-168-629-15

Query Match 11.7%; Score 437.5; DB 4; Length 756;
 Best Local Similarity 23.5%; Pred. No. 1.5e-30;
 Matches 187; Conservative 118; Mismatches 308; Indels 183; Gaps 27;

9 WHTDLLGGAGATASYKARKKSGEYVAVKFNASAYRRPPEVQVREFEVLRNLHNIY 68
 15 WEKKEKLTGCGFNGVIRHNOETGEIOAIKOCROELSPNRREWCLEIQIMRLTHPNV 74
 69 KLFAYEE---TGSROKVLIMEYSSGSLSLVLEDPENTFGLSEEFVLVLCVYAGMN 124
 75 AARDVPEGMONTLPNDLPFLAMEYCGGDLRKYLNOFENCGLREGAILTLSDIASALR 134
 125 HLRNGIVHRDIKPGNIMLVGEEGSIYKLSDFGAARKLDDKVFVSYGTEYLHPDM 184
 135 YLHNRNIHRDLKPNIVLQOGEQ-RLIHKIIDLGAKELDQGSICTSFVGTIQYLAPEL 193
 185 YERAVLRKPOQKAFVTVDMISGVTLYHAATGSLPFIPEGP-----RRNKEIMYRI 237
 194 LE-----QOKYTVTVDMISGVTLYHAATGSLPFIPEGP-----RRNKEIMYRI 245
 238 TTEKPAIGASITGOKONGLEMSYSLPTCRLSMGLQNOVLPIANIL-----EVEEDKC 292
 246 SEDL-----NGTVKFSSSLPTYPNNLNSVLAERLEKWLQMLMWHPRQGTPT 293
 293 WGFDOFAETSDILOTVIHVESLPQAVLHNYIHANHTIAFLVAVYEOTNTPRKHOEY 352
 294 YGNGCGFKALDDILNKLIVHILMTGTIHTYPTEDSLSQAKARIQDDTGIPREDELT 353
 353 LFEGRHCVLPELSAOHIA-----HTAASPFLTFSSSDTPRGKLAFRDPAIDVPRV 405
 354 LQAGLALIPDKPATQICISGKLNIGHTLDMDLVFLFNSKITTEYQISPRQ---PESV 410
 406 -----PKVDLQADYSTAGVLAGYQALMLARVLLDQALMLGLHW-VLEVLODPTCOQ 458
 411 SCILDEPKRNL-AFQOLRK-----VW-----GQVHNSIQTLKEDCNR 446
 459 TLEVTRTALLYL-----GSSIGTERFSSSGMPDV----- 488
 447 LQOGQRAAMNMLLRNNSCKSKMNSMASWSQOLKAKLDFEFTSIQIDLEKYSQTEFGIT 506
 489 -----QERKEATEL---RTRIQTLSEILSKSHNVTETORS-----LSCIGEE 528
 507 SDKLLAMREMEQAVELCGRENEVKLLVERMALQTDIVDLORSPPGRKOGGTLDDLEQ 566
 529 LL-----KNRDOIHEDNKS-----IQKIQCCLDKMHFITYQOKFSRRMRFGLSYNEE 574
 567 ARELYRRLREKPRDQTEBDSQEMVRLILQAIQSFEKKVRYIYTOLSKT-----VVCOK 621
 575 QIHKLKDVNFSLAKRLLOVFOECVQYQVSLVYTGKR--NRQVRAQANHL-HLIGHV 631
 622 ALELLERKLV-----EEV-----VSLMNEDEKTVYRLQEKRKELMNLKIC 662
 632 ATCNSEARGAQLINKIPDOLLDRASEQAGAEVSPQMA-----PHGPRPKDVLVFMQEL 687
 663 SKYRGVSSPSDSMN-----ASRLSQGQLMSQSPSTASNSLPEAKKSEELVAFANHL 715
 688 CNDKMLAFDLDNNR 703
 716 CT---LLENALIDPTVR 728

ATTORNEY/AGENT INFORMATION
NAME: OSMAN RICHARD A

ATTORNEY/AGENT INFORMATION
NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: T97-008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ. ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 745 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-887-518-3

Query Match 9.6%; Score 356.5; DB 2; Length 745;
 Best Local Similarity 22.6%; Pred. No. 2,7e-23;
 Matches 175; Conservative 115; Mismatches 296; Indels 187; Gaps 35;

QY 9 WHTDLLGOGATASVYKANKKSGEVAVAKVENSASYRRPREVQVREFEVLRRLNHNQIV 68
 DB 15 WEMRERLGTGGFNCVLCYOHRELDLKAISKRLSTKRRMCHHEIDIMKLNHANVY 74
 QY 69 KLFVETGSGRQKVL-----MEYSSGSLSVLEDPENPFGLSEEFVLVLCVYA 121
 DB 75 KACDVE-----ELNLIHDVPLAMEYCSGGDLRKLNKPCNGCGIKESQILSLSDIGS 130
 QY 122 GNNHLRENGIVHRDIKPGNIMRLVGEOSIYKLSDFGARKLDDDEKFSVYGTGEYLH 181
 DB 131 GIRYLHENKIHRDLKRENIY-LQDVGKIKIHKIIDLGAKVDGSGISCTSPVGLQYLA 189
 QY 182 PDMEYAVLRKPOQKAFGVTVLMSIGVLYHAATGSLPFI-----PFGPRRKEIMYRI 237
 DB 190 PELFE-----NKPRTATVDYWSFGTVFECIAGYRFLNHLQFTWHEKIK----- 235
 QY 238 TTEKPAIGASTOKENGLEWMSYSLP-----ITCRLSMGLOQLVPLIAN-----I 284
 DB 236 --KDDKCIACEEM-SGEVRESSHLRPNISLCSLIVERMENLQMLNMDPOQGGPVD 292
 QY 285 LEVEDKCGWGFDOFAETSDILQRTVIVHFSLPQAVLHNHYIHAHNTAIFLEAVYEQTN 344
 DB 293 LTLKOPRC-----FVLMHILMLKIVHILNMTSAKITSFLRPDSLSLSQRIERETG 346
 QY 345 VTPKHQEVLEF-----GHPCVLEPSLSAQHI-----AHTAASSPLTLEMSSD 387
 DB 347 INTGSELLSETGISLDPKRPASQCVLDGVRGDSYMYVLFDKSKTYVREGPFASRLSDC 406
 QY 388 TPKGLAFRDPALDVPKF-VPKV-----DLQADYSTAKVGLAGYDALMLARVLDG 437
 DB 407 V--NYVQDSKIQLPIQLKVAEAVHYVSGIKEDYSR-----LEFG 447
 QY 438 Q-ALMLRGLHM--VLEVLQDTCCOOLEVTRTALLYLGS--LGTERRFSAGSGMPDQERK 492
 DB 448 ORAMLSLRLYNANLTKMKWTLSASQOLKAKLEFFHKISIQDLERYS-----EQMT 499
 QY 493 EATELTRQTLSEILSKSHNTEYORSLSCEELKRNQDIHEDNS-----I 543
 DB 500 YGTSSEKMKAKWMEBEKALHYA--EYGVIGYLEDDQIMSLMEIMELQKSPYRGROGDIM 557
 QY 544 QKI-OCCLDMHFITYOKFSKMRPG-LSYNEQ-----IKHLD-----KYNFSLAK 589
 DB 558 ESELOPAID---LYKOLK---RPSDHSYSDSTEWKIIIVHVSQDRYLKRFHSL 610
 QY 590 RL-----LOVFEQEVQYQVSLVTHGKRMROYORAQNIHLIGHSVATCNSE 637
 DB 611 LILCKOKIIDLPKVEVALSNIKEDNTVFMQGRKREL-----WHLL--KIACQSS 662
 QY 638 ARGAQESLKNITFQDLDDRASEGAEVSPQ---NAPHEGPRDKDLYVHQL 687
 DB 663 ARS-----LVGSSLEGA-VTPQAVAMLAP-----DLAEHDHSL 694

RESULT 15

US-09-023-321-3
 Sequence 3, Application US/09023321
 Patent No. 5844073

GENERAL INFORMATION:

APPLICANT: Roche, Mike

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,321

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/887,518

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ. ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-023-321-3

Query Match 9.6%; Score 356.5; DB 2; Length 745;
 Best Local Similarity 22.6%; Pred. No. 2,7e-23;
 Matches 175; Conservative 115; Mismatches 296; Indels 187; Gaps 35;

QY 9 WHTDLLGOGATASVYKANKKSGEVAVAKVENSASYRRPREVQVREFEVLRRLNHNQIV 68
 DB 15 WEMRERLGTGGFNCVLCYOHRELDLKAISKRLSTKRRMCHHEIDIMKLNHANV 74
 QY 69 KLFVETGSGRQKVL-----MEYSSGSLSVLEDPENPFGLSEEFVLVLCVYA 121
 DB 75 KACDVE-----ELNLIHDVPLAMEYCSGGDLRKLNKPCNGCGIKESQILSLSDIGS 130
 QY 122 GNNHLRENGIVHRDIKPGNIMRLVGEOSIYKLSDFGARKLDDDEKFSVYGTGEYLH 181
 DB 131 GIRYLHENKIHRDLKRENIY-LQDVGKIKIHKIIDLGAKVDGSGISCTSPVGLQYLA 189
 QY 182 PDMEYAVLRKPOQKAFGVTVLMSIGVLYHAATGSLPFI-----PFGPRRKEIMYRI 237
 DB 190 PELFE-----NKPRTATVDYWSFGTVFECIAGYRFLNHLQFTWHEKIK----- 235
 QY 238 TTEKPAIGASTOKENGLEWMSYSLP-----ITCRLSMGLOQLVPLIAN-----I 284
 DB 236 --KDDKCIACEEM-SGEVRESSHLRPNISLCSLIVERMENLQMLNMDPOQGGPVD 292
 QY 285 LEVEDKCGWGFDOFAETSDILQRTVIVHFSLPQAVLHNHYIHAHNTAIFLEAVYEQTN 344
 DB 293 LTLKOPRC-----FVLMHILMLKIVHILNMTSAKITSFLRPDSLSLSQRIERETG 346
 QY 345 VTPKHQEVLEF-----GHPCVLEPSLSAQHI-----AHTAASSPLTLEMSSD 387

Db 347 INTGSELSETGISLDPKPKASQCVLDGRCDSYMYLFPDKSKTYEGPFPASRSLSDC 406
QY 388 TPKGLAFDPALDPKPF-VPKV-----DLQADYSPAKGVLGAGYQALWLARVLLDG 437
Db 407 V--NYIVQDSKIQLPYIQLKRYMAEAVHYVSGLKEDYSR-----LFG 447
QY 438 Q-ALMLRGLHW--VEVLQDTGQQTLEVTALLYLGS--LGERFSSGSGMPDVQERK 492
Db 448 ORAMLSLRYNANLTKMKNTLISASQQLKAKLEFFHKSIQDLERY-----EQWT 499
QY 493 EATELTRLOTLSELKSCSHNVTETQRLSCLGEBLLKNRQIHEDNKS-----I 543
Db 500 YGJSSEKMLKAWKEMEKAHYA--EVGVIGYLEQIMSLHAEIMELQKSPYGRQGDIM 557
QY 544 OKI-OCCLDKMHFIYKQFKSRMRPG-LSYNDEQ-----IHKLD-----KVNFSHLAK 589
Db 558 ESLEQRAID---LYKQLKH---RPSDHSYSDSTEMKTIYHTVOSQDRVYLKERFGLHSK 610
QY 590 RL-----LOVFQECVQTYQVSLVTHGRMRQVQRAONHLHLIGHSVATCNS 637
Db 611 LIGCKOKIIDLPKVEVALSNIKADNVMFMQGRKQKEI-----WHLL--KIACQSS 662
QY 638 ARGAGQESLKKIFDQLLDPRASFOGAEVSQP---WAPHPGPPKDLVFRHMEEL 687
Db 663 ARS-----LVGSSLEGA-VFPQAYAWLAP-----DLAEHDHSL 694

Search completed: May 14, 2002, 19:11:34
Job time: 5881 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 14, 2002, 19:12:58 ; Search time 76.26 Seconds

(without alignments)
903.436 Million cell updates/sec

Title: US-09-582-397a-4

Perfect score: 3726
Sequence: 1 MASTNYLMHTDILGOGAT.....LDNNRLIERLHRVSPADV 717

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database : PIR_71:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	354	9.5	745	1	I49101 conserved helix-lo
2	299.5	8.0	1051	1	JW0051 serine/threonine-s
3	293	7.9	1097	2	F96538 hypothetical prote
4	286.5	7.7	1231	2	T18532 serine/threonine pr
5	285	7.6	706	2	A48084 STE11 protein kina
6	279	7.5	1006	2	T26770 hypothetical prote
7	278.5	7.5	795	2	S30874 hypothetical prote
8	278	7.5	974	2	S15038 cell division cont
9	276	7.4	1062	2	S46367 protein kinase CDC
10	272	7.3	774	2	I48609 protein kinase CDC
11	272	7.3	1142	2	S59359 probable serine/th
12	271	7.3	348	2	T37321 GIM protein - yea
13	271	7.3	713	2	S27966 probable serine/th
14	271	7.3	863	2	C88546 protein R107.4 [lm
15	270.5	7.3	560	2	S57252 probable serine/th
16	270.5	7.3	915	2	S74283 probable serine k
17	269.5	7.2	480	2	S56639 ribosomal protein
18	269.5	7.2	733	1	B30001 ribosomal protein
19	269	7.2	735	2	I51901 ribosomal protein
20	268	7.2	465	2	S68462 protein kinase ATP
21	265.5	7.1	629	2	A30001 ribosomal protein
22	265.5	7.1	745	2	G01025 serine/threonine p
23	265.5	7.1	836	2	B96716 probable serine/th
24	265.5	7.1	1906	1	S68235 myosin-light-chain
25	265.5	7.1	2783	2	T34416 hypothetical prote
26	265	7.1	1192	2	T18611 probable serine/th
27	265	7.1	1246	2	D89287 protein H39E23.1
28	264	7.1	1032	2	D83637 serine/threonine p
29	262.5	7.0	257	2	G84797 probable protein k

30	261.5	7.0	856	2	T43631 serine/threonine k
31	260.5	7.0	356	2	T48206 protein kinase ATN
32	260.5	7.0	560	2	T14616 hypothetical prote
33	260.5	7.0	1233	2	T14157 serine/threonine p
34	260	7.0	489	2	T04862 probable serine/th
35	259.5	7.0	658	2	T39500 serine/threonine-s
36	259	7.0	435	2	E84707 protein kinase C (
37	259	7.0	918	1	I48719 protein kinase ATP
38	258.5	6.9	471	2	S68463 myosin-light-chain
39	258.5	6.9	1176	2	JN0583 projectin - fruit
40	258.5	6.9	658	2	T13931 ribosomal protein
41	258	6.9	733	2	A57459 protein kinase RAD
42	258	6.9	821	1	A39616 protein kinase SK2
43	258	6.9	1206	2	T34021 myosin-light-chain
44	257.5	6.9	608	2	A35021 protein kinase C (
45	257	6.9	912	1	A53215

ALIGNMENTS

RESULT 1	149101	conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse
C:Species:	Mus musculus (house mouse)	
C:Date:	10-Sep-1999	#sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession:	I49101	
R:Mock:	B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.	
Genomics:	27, 348-351, 1995	
A:Title:	CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 27.	
A:Reference number:	I49101; MUID:9604444	
A:Accession:	I49101	
A:Status:	preliminary; translated from GB/EMBL/DBJ	
A:Molecule type:	mRNA	
A:Residues:	1-745 <RES>	
A:Cross-references:	EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493	
C:Genetics:		
A:Gene:	CHUK	
C:Superfamily:	mouse conserved helix-loop-helix ubiquitous kinase; protein kinase hom	
C:Keywords:	ATP; phosphotransferase	
F:13-283/Domain:	protein kinase homology <KIN>	
Query Match	9.5%; Score 354; DB 1; Length 745;	
Best Local Similarity	22.0%; Pred. No. 6.3e-10;	
Matches	174; Conservative 125; Mismatches 319; Indels 172; Gaps 30;	
QY	9 WHRDDILGGGATASVYKANKKSGEVNAVKYFNSSA SYRRPEVOYREFVRLKLNHONTV 68	
DB	15 WENREKLTGGFGGNVSLYQHRELDLKIATKSCRLLESSNNRRMCHEIOIMKRLDHANV 74	
QY	69 KLFVEETG---SRQKVLIMEYCGSSLSLVEDPENFFGSEEFVLVLRVAGNMH 125	
DB	75 KACDVEELNPLINDVPLAMCYSGGDLRLKLNPNCCGKLEQOILSLSDISGTRY 134	
QY	126 LBNGLIVHDIPGNIMRLVGEESITVLSDFGAARKIDDEKVSVYGEYVLPDMY 185	
DB	135 LHNKLIHRLDLPENIV-LQDVGGRTIHKIIDLGAKDVQDSGLCTSEFGIYLAPELF 193	
QY	186 ENRVLKPKQKAGVYVDMSIGVTLVYHAAAGSLPFI---PEGPRRKELMYITTEK 241	
DB	194 E-----NKPYTATVDVWSFGTWVFECTIAGYRPLHLHLPYHHEKIK-----RK 237	
QY	242 PAGAISGTQKQENGLPMSYSLP---ITCRLSMGLQNLVPLIAN-----ILEVE 288	
DB	238 DKPCIFACEEM-TGEVRFSSHLPPQNSLCSLVEPMESNLQMLMMDPQQRGCPIDTLK 296	
QY	289 EDKMGCFQFPFETSIIQRTIVYHPSLPQAVLHHVYTHAHTTIAFLBAYEQTNTVPK 348	
DB	297 QPRC-----FALMDHILMLKIVHILNMTSAKIIISFLPCDESLSLQRIERTGTWG 350	
QY	349 HOEYLF-----GHPCVLEPSSLASQHT-----AHFAASSPLTLFSSSDTPKG 391	

Db 351 SEELLSEIGISLDPRKPAQCVLDGRCDSYVYLFDKSKTVYHGPASRSLSDCV--N 408

Qy 392 LAFRPALDVPKPF-VPKV-----DLADYSTAKGVLAGYQALMLARLIDGQALM 441

Db 409 YIVDSKIDLPILQIRKVAEAVHYVSGLKEDYSR-----LFGQRAAMIS--LLEKYNAL 462

Qy 442 LAGLHWLEVLADTCQOILEVTRTALVYIGSSLGTERSSGS--GMPDQERKEATELRT 499

Db 463 TKMKNTLISASQO-LKAKLEFFRKSI-----OLDERYSEQMTYGISSEKMLKAKKEHE 516

Qy 500 RLQTLSEI-----LSKSHNTETORS-----LSGLGEL-----LKNR-- 533

Db 517 KAHISEVAVIGYLEQIIMSLTFETIMELQKSPYGRQGDLMESLQRAIDLYKKLKHRRP 576

Qy 534 DOIHEQNSIQIOCCLDKMHFIYKQFKKSRMRPGLSYNEEQIHLKDYVESHAKRL-- 591

Db 577 DHLYSSTEMVKI-----LVHTVQSO-----DVLKELFEHLKSLKLG 614

Qy 592 -----LQVQEECYQTQVSLVTHGKRMROYORQNHLLIGHSVATCNSEARGA 641

Db 615 KKKIIDLPRKVEVALSNIKEDNTVMFMQGRKKEI-----WHLL--KIACTQSASRL 666

Qy 642 QES-----LNKIFDLDLRASEGAEVSPQMAPHPGDPKDLVFHMOELCNMK 692

Db 667 VSSSLEGTTPPVSAMLPPTLADREHPLTCVTPQ-----DEDTLAQMITEENLCLG 718

Qy 693 LIAFDLDNN 702

Db 719 HLSTIREAN 728

RESULT 2

JM0051
serine/threonine-specific protein kinase (EC 2.7.1.1-) UKL1 - mouse
N:Alternate names: protein kinase UNC-51-like
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JM0051
R:Yan, J.; Kuroiwa, H.; Kuroiwa, A.; Matsuda, Y.; Tokumitsu, H.; Tomoda, T.; Shitara, M.; Bloch, R.; Res. Commun. 246, 222-227, 1998
A:Title: Identification of mouse UKL1, a novel protein kinase structurally related to C.
A:Reference number: JM0051; MUID:98262945
A:Accession: JM0051
A:Molecule type: mRNA
A:Residues: 1-1051 <YAN>
A:Cross-references: GB:AF053756; NID:93136153; PIDN:MAC40118.1; PID:93136154
C:Genetics:
A:Map position: 12q16.3
C:Superfamily: mouse protein kinase UKL1; protein kinase homology
C:Keywords: phosphotransferase
F:14-278/Domain: protein kinase homology <KIN>

Query Match 8.0%; Score 299.5; DB 1; Length 1051;
Best Local Similarity 24.2%; Pred. No. 3.7e-07;
Matches 108; Conservative 60; Mismatches 148; Indels 131; Gaps 14;

Qy 13 DLGGGATASVYKANKKSGEV-VAVKVPNSASTYRPEVOYREFEVLRLNHNQIVLF 71

Db 20 DLGGGATASVYKANKKSGEV-VAVKVPNSASTYRPEVOYREFEVLRLNHNQIVLF 71

Qy 72 AVEETGSGKQVLMVYSSGSLSLVLEDPENTFGLSEEFVLVLRCAVYAGNHNRENGI 131

Db 80 DEQEMANS--VYLVEYKCGGLADYLHTMRT--LSDDYVRLFLQOITAGAMRLHLSKGI 134

Qy 133 VHRDLPKGNIMRLVGEQOSI-----YKLSDFGARLDDDEKRVSYVTEYLHPMY 185

Db 135 IHRDLKPNQIIL-LSNPGGRANPSNIRKYLADFGARLLOSMMMAATLCGSPMTAPRYI 193

Qy 186 ERAVLRRPOQKAFGYTVLMSIGVTLVYHAATGSLPFIFPGGRNKEIMYRITTEKPPGA 245

Db 194 -----MSQHYDGKADLMSTIGTIVYQCLTGKAPF-----QASSPDRLRLFYKNNLT 239

Qy 246 ISGTOKQENGLFLEMSYSLPITCRSLMGLQNLQNVLIANILEVERDKMGCFDEFAETSDI 305

Db 240 VPAPRETSARLR-----QLLALLQNRHKMDDEFF----- 273

Qy 306 LQRTVIVHFSLPQAVLHHVYTHAHNTAILEAVEQETVTPKHQEYLFEGHPCVLEPSL 365

Db 274 -----HHPFLDASTPI-----KSPVPVPSY 295

Qy 366 -----SAQHTAHTAASPLTFM-----SSDPK 391

Db 296 PSSSGSSSSSSSSASHLA-----SPSLGEMPOLQKLTSPADAAAGLQGRSDSGSSKD 350

Qy 392 LAFRPALDVPKPFVPKVDLQADYSTAK 418

Db 351 SCDTDFVMPVPAQPPG-DLVAEASAK 376

RESULT 3

F96538
hypothetical protein F1413.15 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96538
R:Heo, J.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, U.; Cohen, N.E.; Hughes, B.; Huizart, L.
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Liu, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marzla, R.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F96538
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1097 <STO>
A:Cross-references: GB:AE005173; NID:95734778; PIDN:AAD50043.1; GSPDB:GN00141
C:Genetics:
A:Gene: F1413.15
A:Map position: 1

Query Match 7.9%; Score 293; DB 2; Length 1097;
Best Local Similarity 32.6%; Pred. No. 7.9e-07;
Matches 70; Conservative 50; Mismatches 75; Indels 20; Gaps 8;

Qy 9 WHDLDLGGATASVYKANKKSGEVAVK-VRNSASTYRPEVOYREFEVLRLNHNQI 67

Db 6 YHIVELVGESEFGVYGRKRYTGQIVAMKFINQKQRTDIDSLQRETEILKLNHNT 65

Qy 68 VKLFAVEETGSRQKVLIMEYSSGSLSLVLEDPENTFGLSEEFVLVLRCAVYAGNHNH 127

Db 66 IEM-LDSFENAREFCVTFE-AGELFEILEDDK--CLPEQVQAIKQVKAIDYLA 119

Qy 128 ENGIVHRDLPKGNIMRLVGEQOSIYKRLSDFGARLDDDEKFEV-SYVTEYLHPMY 186

Db 120 SNRIHRDMKPNQI-LIG-AGSVKLCDFGARAAMSTVTVALRSIKGPIYMAPELV 174

Qy 187 RAVLRKPOQKAFGYTVLMSIGVTLVYHAATGSLPF 221

Db 175 -----KEQPYDRTVLMSTIGVTLVYGGPPF 202

RESULT 4

serine/threonine protein kinase - guinea pig
N:Alternate names: STE20-like kinase
C:Species: Cavia porcellus (guinea pig)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: T18532
R:Itoh, S.; Kameda, Y.; Yamada, E.; Tsujikawa, K.; Mimura, T.; Kohama, Y.

[illegible]

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26770
R: Smye, R.
submitted to the EMBL Data Library, September 1999

A:Reference number: 220262
A:Accession: T26770

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-1006 <WIL>

A:Cross-references: EMBL:AL110482; NID:e1542197; PIDN:CAB54389.1; CESP:Y3968B.e
A:Experimental source: clone Y3968B

C:Genetics:
A:Gene: CESP:Y3968B.e

A:Introns: 138/1; 205/3; 475/3; 713/2; 747/3; 835/2; 897/2

Query Match 7.5%; Score 279; DB 2; Length 1006;
Best Local Similarity 22.2%; Pred. No. 3.4e-06;
Matches 165; Conservative 124; Mismatches 255; Indels 198; Gaps 38;

```

OY 7 YLMTDDLLGOGATASYKARKKSGEVAVKVF--NSASYRPPPEVYREFEVLRLNH- 64
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 19 YLYNDEFPAKAGASQVYRGR-ESGRVAVKATKATSKADVDAMCTEIDILKLGCV 77
OY 65 ONIVLFAVEETGSGROVLI-----MEYSSGSLSVLEDPENTFGLSEEFV-LVLR 117
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 78 ANIVYFESKNTKIPPGSVTITETISFAME-CASRSLDAEMRPERNHKGLPSNVLIDLYVD 136
OY 118 CVVAGMNLRENGIVHRDIKPGINRLV-----GEGQSITKLSDFGARKLDD--EKF 170
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 137 CSMA-LSALREHNLARHDKIMNILLFGSPTRGRSTHLKLCDMGCSKAISENSOEL 195
OY 171 VSVYTEEYLPD-----MERAVALRKPOOKAFGVTVLMSIGVTLVYHAATGSLPFI 223
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 196 NSIACTKTFPLDHPNGHMKTKSAVTPQ-----CDLMSIGCTLYFCATGEPPF-- 247
OY 224 FGPPRNKEIWRIT-----TEKPAGALSCTOKONG-----PLEWS--YSL 263
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 248 --ESTRADANILYHMAADLTNPANAVANLVQVENPVTKERKVFEPYTELPAPETRYPK 305
OY 264 PITRCLSMGLN-----OLVPI-----LANLE--V 287
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 306 WLVTMTCLRNFPHERPSIEYKAVAGMNRKRTFASVDQMSIVETDMSNLESPL 365
OY 288 EEDCKGFDQ-----FPAETS-----DILQRTVHVESLPOAVLHNYIHAHT-- 331
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 366 SISCLGPEGIDIVLANSTHYLDSKOKS--VDGLPD--DLYLVLPQTSQVEMRT 418
OY 332 -----TAIFLEAVYEQTNVTPKHQEV--LFEGRPVLEP--SLSAQ 368
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 419 LKRNKIFNELECMTDTKLEIRIKCEGLSMLEVEYDLDFRVSALLSTQFSILVQ 478
OY 369 HIAH-----TAASSPLFLFSMSDTPKGLAER--DPALDVKFPYK-VDIQ 411
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 479 ELISQFEVQTTSRPAAVYVDASVPMMLFDEANPEAKTIADQIQQAQAEELERAKVA 538
OY 412 ADYSTAGVAGAGYQALMLARVLLDGOALMLRG-LHWVLEVLQDTQCOQTEVTRIALLY 470
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 539 MDPFACAKKISREARDELRLDMQDPLGRRETESLYFLPYDKATYLLSTQYQELVELCLIKR 598
OY 471 GSSLGTERFSSGSGMPDVERK-----EATELTRRLQTLSELISKSHNVTEORS 521
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 599 NTYVA-KOIFNSPDG--INRSKINTAMNLAASLSQLRSDVQKQDMISEC----- 644
OY 522 LSLGSELLKNRQIHED--NKSIOKIQCCLD--KMHFIYKQFKSRMRPGLSYNEQO 575
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 645 -----VDLEKPPQVAKDNNRYLQAGCSRNTEKSMHLLRPFENQIR--MKSTHS 697
OY 576 IHLT-DKVNFSHLAKRLLOVFO 596
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 698 CKRLIDQLN-----KELEQIQ 714

```

RESULT 7

S30874

hypothetical protein R107.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Feb-1997

C:Accession: S30874

R: Thomas, K.

submitted to the EMBL Data Library, July 1992

A:Reference number: S30871

A:Accession: S30874

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-795 <THO>

A:Cross-references: EMBL:214092

C:Genetics:
A:Genetic code: SGCA

A:Introns: 170/1; 237/3; 518/3

C:Keywords: serine/threonine-specific protein kinase

Query Match 7.5%; Score 278.5; DB 2; Length 795;
Best Local Similarity 21.8%; Pred. No. 2.8e-06;
Matches 168; Conservative 122; Mismatches 275; Indels 207; Gaps 37;

```

OY 7 YLMTDDLLGOGATASYKARKKSGEVAVKVFNSASIRRPPEVYREFEVLRL-NHQ 65
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 55 YTFNDSISKAGVSEYVSGRT-ESGSLAVK--TACKKLEVAAMGEIILKIKIGAS 110
OY 66 NIVKLFVEETGSGROV-----LIMEYSSGSLSVLEDPENTFGLSEEFV-LVLR 118
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 111 NIVYFESGNTKMAPGSVTSSETISFAMEYASS-SLEAKMSRNHSGLSNALIDLYVDC 169
OY 119 VVAGMNLRENGIVHRDIKPGINRLV-----GEGQSITKLSDFGARKLDD--EKF 171
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 170 SMA-LSALREHNLARHDKIMNILLFGSPTRGRSTHLKLCDMGCSKASENSHEMS 228
OY 172 SVYCTEELHP-----DMERAVLR-----KPOOKAGVYVDMSIGVTLVYHAATGSLPFI 222
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 229 TLVGTNLLHPLFAHMDVPLMAQNSHMKTKSATVSECCDLMAIGCTLYFCATGEPPF 288
OY 223 PEGGPR-----RNKEIWRITTEKPAGALSCTOKONGPL-----EWS 260
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 289 HESNNKSLYHKAVALTQNDALAMLVOKGRDPGSSDTMPEFQVTELPKFTSYPKVL 348
OY 261 YSLPITCRLSMGQNLVLIANILE-----VBE----- 289
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 349 VS-TMTCILRSFHERPSIEYKAVADAMNSKRSFSSVDQMSIVETDMSNVPLGFSI 407
OY 290 --DKCWGFDQ-----FPAETS-----DILQRTV-----IHVESLPOAVLH 323
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 408 PISIKCLGPEGIDIVLANSTHYLDSKOKSVQDGLPDDLIVYVQTSHV-DMSKILSN 466
OY 324 VYIHAHTTA-----IFLEAVYEQTNVTPKHQEV--LFEGRPVLEP--SLSAQHIA-- 371
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 467 IEFHERDDMTSKLEIRIKCEGLSMLEVEYDLDFRVSALLSTQFSILVQELSQF 526
OY 372 ---HTA-----ASSPLFLFSMSDTPKGLARFDALDVPKVRK-----VDLQDY 414
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 527 EKVQTAASRAVYVDASVPMMLFDEAN--PETKMISDQIOAKASAELESNAKVSMDI 584
OY 415 STAKVYLACGYQALML-----ARVLLDGOALMLRGVHWVLEVLQDTQCOQTE 470
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 585 EACARQLSKDAEDRLLEMDLPGICEIESYVYFQKAIL-----STQKYSQELVE 635
OY 462 VTRTALLVGSISGTERFSSGSGMPDVERK-----EATELTRRLQTLSELISKSHNV 515
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 636 L-----KLSNNIMQOIFNSPDQSNKSKLNAKMLAASLSQLRSDVQKQDMISEC----- 687
OY 516 TETQSLSGEELLKNRQIHED--NKSIOKIQCCLD--KMHFIYKQFKSRMR-- 566
    | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 688 -----VDLEKPPQEMKQDVNRYLQAGCSRNTEKSMHLLRPFENQIR--MKSTHS 736

```

QY 567 --PGLSTNEQIIH-KIDKVNESHAKRLLOVFE-----ECVQTVQVSLVT 609
 Db 737 TTKSCSKLIDQLMELDQLGFVRLGDMILIKASEQQLTSSEETIOVQVSVS 788

RESULT 8

cell division control protein CDC15 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YAR019c
 C:Species: Saccharomyces cerevisiae
 C>Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 24-Sep-1999
 A:Accession: S15038; S43213; S25680; S40907; S20124; S23678; S43452
 R:Schwartz, B.; Phillips, P.
 A:Title: CDC15, an essential cell cycle gene in Saccharomyces cerevisiae, encodes a prot
 A:Reference number: S15038; MUID:91353080
 A:Accession: S15038
 A:Molecule type: DNA
 A:Residues: 1-974 <SCH1>
 A:Cross-references: EMBL:X52683
 R:Schwartz, B.
 Submitted to the EMBL Data Library, May 1993
 A:Reference number: S43213
 A:Accession: S43213
 A:Molecule type: DNA
 A:Residues: 1-899, 'KDV', 903-974 <SCH3>
 A:Cross-references: EMBL:X52683; NID:g298029; PIDN:CAA36906.1; PID:g298030
 R:Schwartz, B.
 Submitted to the EMBL Data Library, August 1991
 A:Reference number: S25680
 A:Accession: S25680
 A:Molecule type: DNA
 A:Residues: 1-974 <SCH>
 A:Cross-references: EMBL:X60549
 R:Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.; Zeng, B.; Delaney, S.; Que
 Submitted to the EMBL Data Library, November 1993
 A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: Analysis of the 4
 A:Reference number: S40907
 A:Accession: S40907
 A:Molecule type: DNA
 A:Residues: 1-974 <CIA>
 A:Cross-references: EMBL:L22015; NID:g1339990; PIDN:AAC04565.1; PID:g349757; MIPS:YAR019
 R: Davies, C.J.; Hutchison III, C.A.
 Submitted to the EMBL Data Library, January 1992
 A:Description: A directed DNA sequencing strategy based upon Trn3 transposon mutagenesis:
 A:Reference number: S20123
 A:Accession: S20124
 A:Molecule type: DNA
 A:Residues: 865-899, 'KDV', 903-974 <DAV>
 A:Cross-references: EMBL:M67445; NID:g170997; PIDN:AAA34400.1; PID:g171001
 R:Schwartz, B.; Phillips, P.
 Mol. Gen. Genet. 234, 164-167, 1992
 A:Title: NPKL, a nonessential protein kinase gene in Saccharomyces cerevisiae with simil
 A:Reference number: S23580; MUID:92357012
 A:Accession: S25678
 A:Molecule type: DNA
 A:Residues: 941-974 <SCH2>
 A:Cross-references: EMBL:X60549
 R:Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Fortin, N.; Zeng, B.; Delaney, S.; Que
 Yeast 10, 535-541, 1994
 A:Title: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 42 kbp
 A:Reference number: S43441; MUID:95028152
 A:Accession: S43452
 A:Molecule type: DNA
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Residues: 1-974 <CLM>
 A:Cross-references: EMBL:L22015; NID:g1339990; PIDN:AAC04565.1; PID:g349757
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
 C:Genetics:
 A:Gene: SGD: CDC15
 A:Cross-references: SGD:S0000072; MIPS:YAR019c
 A:Map position: 1R
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C:Keywords: ATP; serine/threonine-specific protein kinase
 F:23-272/Domain: protein kinase homology <KIN>
 F:31-39/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 21.8%; Pred. No. 3.6e-06;
 Matches 139; Conservative 101; Mismatches 216; Indels 182; Gaps 29;

QY 9 WHRDDLLGGATATPASYKARKKSGEVAVKVNASYSRRPPVQ--VREFEVLRLNHQ 66
 Db 25 YHLKQVIGKSGVGVKAKIKHTDQVVAIK--EYVDEDEELNDIMAEISLKLKLNHN 81
 QY 67 IVKLFVVEEGSGRQKVLIMEXCSSGLSLVLEDPENTFGLEEPLVLRGVAGMNL 126
 Db 82 IVYHGFIRK--SYELVILILEFCANGLRLRLS--RSSGLSENESEKTVVQTGLGAKL 137
 QY 127 RENGIVHRDIKPGINMLRVGEESQSYKLSDFGARKLDDDEKVSVYTEEYLHPDYE 186
 Db 138 HGEVYIHRDIKAMNILL--SADNTVKLADPGVSTIVNSA--LTLAGTLNMAPEIL- 190
 QY 187 RAVLRKPOQKAPGVVDLMSIGVTLNATGSLPFIPEGPRRNKRIMRTTERPAGNI 246
 Db 191 -----GNKGASTLSIDMSLGAIVEMLTKNPY-----NLTP----- 223
 QY 247 SGTOKENGPLEMSYSLPTTCRLSMGLQOLVPIILANI--LEVEEDKMGDFDFAETSPI 305
 Db 224 -----ANIVVAENDIYPPSSSEPLKDF 248
 QY 306 LQRTVI-HVFSLPQA--VLHNYIHAHNTIAT-----FLEAVY-----EQTV 345
 Db 249 LSKCFVKNNYKRPTADQLLKHWINSTENVYKDKLNKFKEDFDADQHWADAFQEEKLNI 308
 QY 346 TPKHQEVLEFGHCY-----LEPSLSAOLIAHTAAS--PLT-----LFSMSDTPKG 391
 Db 309 SP--SFLSRAAPAPPAENNOEIDLMPPTESQLSKSSKPLDHLHFSVCS----- 361
 QY 392 LAERDPAIDVPRFVPIVLDADYSTAKVGLA-----GYQALMLARVLDGQALMLRGLH 446
 Db 362 --LENIADTIECLSRPTVDKRLITAFSGIFVYDQHNHSRLKRFIANGGIPLIKFPH 419
 QY 447 WLEVLQDTCQQLVETRTALLYLGLSSLGERSSSGAPDVQERKEATELRRLQTLSE 506
 Db 420 LAKEFVIDPQTLIE--CGIMF-----PPNPAS-----LTPRYILIELVRFYDL 464
 QY 507 ILKCSHNWTEQRLSCIGELKLRNDQIHENK-----LTPRYILIELVRFYDL 552
 Db 465 TAFWCRCMKFRHNDISL-----LLNN-----IHERAOSILKLSSVAPWSEFKILPSLIDS 515
 QY 553 MHPIYQFKRSRMRPGLSY-----NEEQIHK 578
 Db 516 -----KLKKRIISPDITVYVFKSIVMYMTTNDKIKH 548
 RESULT 9
 S46367
 C:Species: Schizosaccharomyces pombe
 C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 10-Dec-1999
 A:Accession: S46367; T19888
 R:Frankhauser, C.; Simanlis, V.
 EMBO J. 13, 3011-3019, 1994
 A:Title: The cdc7 protein kinase is a dosage dependent regulator of septum formation
 A:Reference number: S46367; MUID:94313982
 A:Accession: S46367
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-1062 <FAN>
 A:Cross-references: EMBL:X78799; NID:g521098; PIDN:CAA5382.1; PID:g521099
 A:Experimental source: wildtype 972 h minus
 A:Note: mRNA sequencing was also done to confirm the intron borders
 R:Saunders, D.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 Submitted to the EMBL Data Library, February 1999

Query Match	7.48:	Score 276:	DB 2:	Length 1062:
Best Local Similarity	26.38:	Pred No. 5e-06:		
Matches 103:	Conservative 64:	Mismatches 130:	Indels 94:	Gaps 16

RESULT	10
I48609	

RESULT 11

G1M4 protein: yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein YDR570c
C:Species: *Saccharomyces cerevisiae*
C:Date: 30-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 24-Sep-1999

Db 580 ERRRRKQEEKERARKLLEKEDLKRKQEEELKKQIEIDISDLQELSKHKEEKL DGNIRSI 63

Db 193 ---QQRPGKAVDWSIGVIAIILLGYPFF 220

E:54-307/Domain: protein kinase homology <KIN>

Query Match 7.3%; Score 271; DB 2; Length 713;
 Best Local Similarity 23.0%; Pred. No. 5.6e-06;
 Matches 169; Conservative 112; Mismatches 262; Indels 192; Gaps 35;

```

QY 15 LGOGATASVYKARKKSGEVAVAVKFNASARYRPEVO--VREPEVLRRLNHNQIVLKA 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 IGGNFAKVKLARHILGREAVALIKIDKQOL-NPTSLQKLFREVRIKILNHPNIVLFE 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 VEETGGSRQKYLIMEYSSGSLVLEDPENTFG-LSEEPVYLRCVAGMHLRNGI 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 VLEF--OKTLYLIMEYASGKVPDYLV---AHGRMEKAKRSKFRQIVSAVOYCHQKRI 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 VHRIRKGNIRLVGEEGOSLYKLSDFGAARKLDDDEKFSVYGTETYLHPDMERAVLR 191
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 VHRDKENLIL---DADNRIKADFGFSNEFTVGKLDTFGSPRYAPBELFQ----- 225
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 KPOKACGVTVLMSIGVTLVHAATGSLP-----IPGGRRNKEI 233
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 226 --GKKYDQPEVDVMSLGVITLYLVSGSLPFDGQMLKELEHRLRGKYRIPFYMSDCE 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 234 MYRTTEKP--AGAI-----SGTQKENGPR-----LEMSYSLPITCRLSMGLQ 276
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 284 LKRLVLPNPIKRGTLQIMKDRMINAGHEDELKPEVEPELIDSDQKRIDIMWGMYSOE 343
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 277 LVPILANILEVED--KCMGFDPFA-----ETSDILQRTVIVFSLPQAVLHHVYIHA 328
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 344 -----ETQESLSKKKAYDEITATYLLGRKSEVRRPSDDL-NSTGSPHHKY----- 389
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 329 HNTAIFLEAVYEQTNTVTKHOEYLFEGHPCVLEPSLSA--QIATAHAPASSPLTFE 386
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 390 -----ORSVSSOKORRYSDHAGPGIPSVAYPKRSQTSADSLKEDGISS 436
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 387 DTP-----KGLFRDPAAL-----DYKFPVPKVDLQADVSTAKGVLAGYQALWL 430
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 437 RKSTGSAVGKGIAPASPLGNASNPKNADTP--RKSSIVPSSSTSGGTRNNITYCS 495
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 431 ARVLIDGQALMLRGLHWLLEVLQDTCCQTELEVTR--ALVLYGSLGTE--RESSGS-- 483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 496 ERTDHRHSYVIONGKE-----NSTIPDQRTPVASTHSSISAAIPRIIRPRGTAS 545
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 484 -----GMPDVORR-----EATEL--RTRLQTLSELSCSHNVTETQSL 522
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 546 RSTFGPQ--RRRTATVNGPPASPSPSLSEATPLSQTSRSTSLFKLTLRIS--RN 602
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 523 SCLGELLKNRDQIHEDKKSIOKIOCCDDKMHFIYKQFKSRMPG----- 568
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 SA-----KQKD-----EKKEAP--RSIRFTMSKMTTSSMDPQDMRIKRVLDANN 647
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 569 LSYNEEQIHLKDKYNSHIAKRLLOVFOECVQTYQVSLVTHGKRMRQVORAQNHLLIG 628
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 648 CDYEQREHFLFCVGHGDAENLVQWEMEVC-KLPRLSL--NGVAFKRIS-----G 695
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 629 HSVATCNSEARGAOF 643
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 696 TSIARFNIAKTIANE 710
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 14

C88546
 Protein R107.4 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: C88546
 R:Anonymous. The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
 A:Accession: C88546
 A:Status: Preliminary
 A:Molecule type: DNA

A:Residues: 1-863 <STO>
 A:Cross-references: GB:chr_III; PIDN:CAA78473.1; PID:g3879038; GSPDB:GN00021; CESP:R1
 C:Genetics:
 A:Gene: R107.4
 A:Map position: 3

Query Match 7.3%; Score 271; DB 2; Length 863;
 Best Local Similarity 21.2%; Pred. No. 6.9e-06;
 Matches 170; Conservative 124; Mismatches 247; Indels 262; Gaps 38;

```

QY 7 YLMTDILLGOGATASVYKARKKSGEVAVAVKFNASARYRPEVOVREPEVLRRL-NHQ 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 55 YTLFNEDESGICKGASVSEVYGR--ESGRLVAVR---TACKLKVAAIGIEIELKRLKAS 110
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 66 NYKLAVEETGGSRKY-----LIMEYSSGSLVLEDPENTFGSEEF--VVLRC 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 NIVQFGSNHTKMAPGSVSETISFAMEYAS--SLAEARRKRNHGLSSNALIDLVDQC 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 VVAGMHLRENGIVHRDIKPGNIMRLV-----GEEGOSLYKLSDFGAARKLDD--EK 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 SMA--LSALREHNIAHRDIKHMNILLFPQPTGRGRSTHLFKLQDMGCKSLSENSHE 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 SVYGTETELHP--DYERAVLR-----KPOKACGVTVLMSIGVTLVHAATGSLP 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 229 TLVGTPLNLLHPFLAHMVDPLMAQNRHNMKTKSAYTSBOCDLALGCTLYFCATGK--F 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 223 PEGGPRRNKEIMYR-----ITTEKPAAGISGTOK-----ENGPL----- 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 PFEHRRNNSLYKAVALLQNDALAMVLVOKGRDPRGRTDIFEPQVTELPKAFTRIP 345
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 258 EMSYSLPITCRLSMGLQNLVPLANILE-----VBE----- 289
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 346 KMLVS--TMTCLLSFHEPSIEYKAVADAMRSKRRTSSVDQMSIVHTDMSNPHLG 404
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 290 -----DKCGFQOFAEISDI--LQRTVYH-----VFSLP----- 317
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 405 FSLPSISKCG-----VPEGDILLNSTHYLDSKQSVGDLPLDLYLVQTSVDNR 460
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 318 QAVLHHVYIHAHNTIA-----IFLAVYEQTNTVTKHOEY--LFEGHPCVLEP--SL 367
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 461 KILARNIEFHPDMMDRKSLRIKCYGSLMLEIDELALFPRVSTILSTQSSLY 520
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 368 QHIA-----HTA-----ASSPLTFSSMSDTPKGLA----- 393
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 521 QELSQEFERYOTASRAVAYVDMASVPLMLEDEANPEKTMISDQIQAKRARELEHNAV 580
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 394 -----FRPALDVPRKVPKY-----DLQADYSPAKGVLAGYQALWL 430
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 581 SMDIEACAKQLSKDAEDLRLEDMDLPGLCEELISYVPYDQALISTOK-----Y 629
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 431 ARVLIDGQALMLRGLHWLLEVLQDTCCQTELEVTRTALLVYSSIGTERFSSGSGMPDVO 490
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 630 SQELVE---LCIKRRNNIMQIIFNSPDRINKSLANKAMNLAASL----- 670
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 491 RKEATELRTQLTSELSCSHNVTETQSLSCLEBELKNRDQIHED--NKSIOKIO 548
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 671 -----SQLRSNVRKLQDMISEC-----VDLEKFPQDMKDVNRYLQAOGC 711
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 549 CLD-----KMHFIYKQFKSRMPGLSYNE-----EQIH-KLQVNSHLAKRLLOVFO 598
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 712 SRNMQKSMHLRREFHESQIRIKKTKSCRLKLDQINIEIDQLGVRIGDILITAESE 771
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 599 CVQTYQVSLVTHGKRMRQVORAQ 621
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 772 TL-----TRSEIDETQ 783
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 15

S57252
 probable serine/threonine-specific protein kinase (EC 2.7.1.-) YGL179c - yeast (Sacch
 N:Alternate names: Protein B1560; protein G1618
 C:Species: Saccharomyces cerevisiae

C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
C:Accession: S57252; S64196; S6168
R:Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Bruschi, C.V.
Yeast 11, 767-774, 1995
A:Title: The DNA sequence of a 7941 bp fragment of the left arm of chromosome VII of *Saccharomyces cerevisiae* and a putative serine/threonine protein kinase gene.
A:Reference number: S57252; MUID:95397594
A:Accession: S57252
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-560 <COC>
A:Cross-references: EMBL:X83690; NID:g794143; PIDN:CA58659.1; PID:g794144
R:Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64196
A:Accession: S64196
A:Molecule type: DNA
A:Residues: 1-560 <BRD>
A:Cross-references: EMBL:Z72701; NID:g1322788; PIDN:CA96691.1; PID:e243787; PID:g132278
A:Experimental source: strain S288C
C:Genetics:
A:Map position: 7L
A:Note: YGL179c
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; transmembrane
F:48-344/Domain: protein kinase homology <KIN>
F:56-64/Region: protein kinase ATP-binding motif
F:256-272/Domain: transmembrane #status predicted <TMM>

Query Match 7.3%; Score 270.5; DB 2; Length 560;
Best Local Similarity 24.1%; Pred. No. 4.5e-06;
Matches 108; Conservative 63; Mismatches 147; Indels 131; Gaps 19;

QY 15 LGGATASYRKANKKSGVVAVKFNASARYRPEVOVR-----EFEYLRRLNHON 66
DB 56 LGGNGYGVKYLARDGTGALVAIKILNFEKRSGLDQKVENPRVNOEIEYMKRCHHEN 115
QY 67 IVKLFVETGGSRQKVLIMEYSSGSLSLVLEDPEN-----TEGLSEEFVY 114
DB 116 VVELEYEILNDPESTKYVLYLECYSGNRG---PVKWCPEKMEIKAVGPSILTFQOSRK--- 168
QY 115 VLRVYVAGMNHLENGIYHRODKPGNIMRVLCEGSGTYKLSDFGAARKL-----DD 166
DB 169 VVLDVYVSGLEYLHSGIYHRODKIPSNL--LISSNG--TVKISDFGVAMSTATGSTNIQSS 224
QY 167 DEKFVS--VGTTEYLHPDMEYERAVLRKPOQKAFGVTVDLMSIGVTLXEAATGSLPIPF 224
DB 225 HEQLKSRALGTAPAFAPFEL-----CSTEKEYSCSSAIDIMSLGVITICLLEFGKLPFNAN 279
QY 225 GGPFR-----NKEIMYRTITTEKPAKAISGTOKOENGPLEWSYSLPTCFLSMGLONQLVP 279
DB 280 SGLLEFLDSIINKPLEFPSEYEEMLNGATSGITMEE-----YTDAKD 319
QY 280 ILANTLEVEEDK-----C-WG-----FDOFFAETSDILQRTVIH 312
DB 320 LKKLLQKDPDPKRIKLADIKVHPFMCYKGSQDASVLTNLETFHLLKVPSPSSCKR--VE 377
QY 313 VESLPQ-----AVLHHVYIYH--AHNTI-----AIFLAVYEQFTVTPKHQEVYLFEGHPC 359
DB 378 LVSLPVSNSFPASLDVYVEMENDHNNLRTGADRNSITYSPIYDANTLSP----- 425
QY 360 VLEPSLSAQHIAHTAASSPLTLFSKSSDP 388
DB 426 -----SAYHNIGSRRESSYSSFSST 448

Search completed: May 14, 2002, 19:13:03
Job time: 775 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2002, 17:32:05 ; Search time 66.66 Seconds
(without alignments)
416.470 Million cell updates/sec

Title: US-09-582-397A-4

Perfect score: 3726
Sequence: 1 MOSTNTNLTMTDLDLGGAT.....LDNNRLIERLHRVSAADV 717

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3726	100.0	717	1 IKKE_MOUSE	Q9ROT8 mus musculus
2	3102.5	83.3	716	1 IKKE_HUMAN	Q14164 homo sapien
3	437.5	11.7	756	1 IKRB_HUMAN	Q14920 homo sapien
4	428.5	11.5	757	1 IKRB_MOUSE	Q88351 mus musculus
5	418.5	11.2	757	1 IKRB_RAT	Q9QY78 rattus norv
6	354	9.5	745	1 IKKA_MOUSE	Q06600 mus musculus
7	352.5	9.5	745	1 IKKA_HUMAN	Q15111 h inhibitor
8	299.5	8.0	1051	1 ULK1_MOUSE	Q70405 mus musculus
9	294.5	7.9	1050	1 ULK1_HUMAN	Q75385 homo sapien
10	288.5	7.7	966	1 ST10_MOUSE	Q50285 mus musculus
11	285.5	7.7	661	1 Y537_HUMAN	Q60285 homo sapien
12	278	7.5	974	1 CC15_YEAST	P27636 saccharomyc
13	277	7.4	968	1 ST10_HUMAN	Q94804 homo sapien
14	276	7.4	1062	1 CC7_SCHRO	P41892 schizosacch
15	274	7.4	1431	1 DAPK_HUMAN	P53355 homo sapien
16	272	7.3	774	1 KEMK_MOUSE	Q05312 mus musculus
17	272	7.3	1142	1 GINA_YEAST	Q12263 saccharomyc
18	271	7.3	713	1 KP78_HUMAN	P27448 homo sapien
19	271	7.3	863	1 YNH4_YEAST	P32742 caenorhabdi
20	270.5	7.3	560	1 KGS9_YEAST	P43637 saccharomyc
21	270.5	7.3	915	1 KC64_YEAST	P25389 saccharomyc
22	269.5	7.2	733	1 K6A1_XENLA	P10665 xenopus lae
23	269	7.2	735	1 K6A1_HUMAN	Q15418 homo sapien
24	268	7.2	465	1 KPK1_ARATH	P42818 arabidopsis
25	265.5	7.1	629	1 K6AB_XENLA	P10666 xenopus lae
26	265.5	7.1	1906	1 KML5_CHICK	P11799 gallus gall
27	264	7.1	487	1 STK4_HUMAN	Q13043 homo sapien
28	263	7.1	424	1 KPSH_HUMAN	P11801 homo sapien
29	263	7.1	1030	1 STR9_HUMAN	Q76039 homo sapien
30	262.5	7.0	714	1 HUNK_HUMAN	P57058 homo sapien
31	261.5	7.0	856	1 UN51_CAEL	Q23023 caenorhabdi
32	260.5	7.0	386	1 KPBG_HUMAN	Q16816 homo sapien
33	259.5	7.0	658	1 PAK1_SCHRO	P50527 schizosacch

34	259	7.0	918	1 KPCM_MOUSE	Q62101 mus musculus
35	258.5	6.9	471	1 KP19_ARATH	Q39030 arabidopsis
36	258.5	6.9	714	1 HUNK_MOUSE	Q88666 mus musculus
37	258.5	6.9	1176	1 KML5_BOVIN	Q28844 bos taurus
38	258	6.9	733	1 K6A2_HUMAN	Q15349 homo sapien
39	258	6.9	821	1 SPK1_YEAST	P22216 saccharomyc
40	257.5	6.9	607	1 KMLC_RABIT	P07313 oryctolagus
41	257	6.9	912	1 KPCM_HUMAN	Q15139 homo sapien
42	256.5	6.9	433	1 ST11_HUMAN	Q15831 homo sapien
43	256.5	6.9	1597	1 M3K4_MOUSE	Q08648 mus musculus
44	256	6.9	1579	1 SSK2_YEAST	P53599 saccharomyc
45	255.5	6.9	406	1 KPBH_RAT	P31325 rattus norv

ALIGNMENTS

RESULT	ID	IKKE_MOUSE	STANDARD:	PRT:	717 AA.
AC	Q9ROT8;	IKKE_MOUSE			
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Inhibitor of nuclear factor kappa-B kinase epsilon subunit				
DE	(EC 2.7.1.-) (I kappa-B kinase epsilon) (IKBE) (IKK-epsilon) (IKK-E)				
DE	(Inducible I kappa-B kinase) (IKK-1).				
GN	IKBE OR IKKE OR IKK1.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Macrophage;				
RX	MEDLINE=99352266; PubMed=10421793;				
RA	Shimada T., Kawai T., Takeda K., Matsumoto M., Inoue J.-I.,				
RA	Tatsumi Y., Kanamaru A., Akira S.;				
RT	IKK-1, a novel lipopolysaccharide-inducible kinase that is related to				
RT	IkappaB kinases.;				
RL	Int. Immunol. 11:1357-1362(1999).				
CC	- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO				
CC	THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND				
CC	ULTIMATELY THE DEGRADATION OF THE INHIBITOR. MAY PLAY A SPECIAL				
CC	ROLE IN THE IMMUNE RESPONSE (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: Cytoplasmic (Probable).				
CC	- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS).				
CC	- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).				
CC	- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
CC	IKAPPAB KINASE SUBFAMILY.				
CC	-----				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AB016589; BAA85154.1; -				
DR	MGI; MGI:1929612; Ikbe.				
DR	InterPro; IPR000719; Euk. kinase.				
DR	InterPro; IPR002290; Ser_thr_kinase.				
DR	InterPro; PF00069; kinase.1.				
DR	Pfam; PF00069; kinase.1.				
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP.1.				
DR	PROSITE; PS00108; PROTEIN_KINASE_SF_FALSE_NEG.				
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM.1.				
KW	Transferase; Serine/threonine-protein kinase; ATP-binding;				
KW	phosphorylation.				
FT	DOMAIN 9 315 PROTEIN KINASE.				
FT	DOMAIN 452 473 LEUCINE-ZIPPER (POTENTIAL).				
FT	NP_BIND 15 23 ATP (BY SIMILARITY).				
FT	BINDING 38 38 ATP (BY SIMILARITY).				

FT	ACT_SITE	135	135	BY SIMILARITY.
FT	MOD_RES	172	172	PHOSPHORYLATION (BY SIMILARITY).
SQ	SEQUENCE	717 AA;	80939 MW;	3863E0A0FAB997D3 CRC64;

Matches 596; Conservative 58; Mismatches 58; Indels 9; Gaps 4;

OY 1 MOSTNYLMTHTDLDLGATASVYARRKKSSGVAVKVSASRRPEVYVREFEYL 60
 DB 1 MOSTNYLMTHTDLDLGATASVYARRKKSSGVAVKVSASRRPEVYVREFEYL 60
 OY 61 RHNHNIYVLFVFEFTGGSRKVLIMEXYSSGSLSVLEDPNTFGLSDEEFLVYRCV 120
 DB 61 KLNHNIYVLFVFEFTGGSRKVLIMEXYSSGSLSVLEDPNTFGLSDEEFLVYRCV 120
 OY 121 AGMNLRENGIYHRDIPKPNIMRLVGEQGSITKLSDFGARKLDDDEKFSVYGTSEYL 180
 DB 121 AGMNLRENGIYHRDIPKPNIMRLVGEQGSITKLSDFGARKLDDDEKFSVYGTSEYL 180
 OY 181 HPDMYRAVLRKPKQAKAFVYVDLMSIGTYLYHAATGSLPFIPEGPRRNKELMTITE 240
 DB 181 HPDMYRAVLRKPKQAKAFVYVDLMSIGTYLYHAATGSLPFIPEGPRRNKELMTITE 240
 OY 241 KPAKATAGAQKRENGPLKEMSTYLPITCOGLSGQSLVYILANILEVEQAKMGDFQFA 300
 DB 241 KPAKATAGAQKRENGPLKEMSTYLPITCOGLSGQSLVYILANILEVEQAKMGDFQFA 300
 OY 301 ETSIDLQRTVHYVSLPQAVLHNYTHAHTTAIFLEAVEYEGTNTPKHOEYLFEGHPCV 360
 DB 301 ETSIDLQRTVHYVSLPQAVLHNYTHAHTTAIFLEAVEYEGTNTPKHOEYLFEGHPCV 360
 OY 361 LEPSTLQNHNTAASSPLTFEIMSDDTPKGLAFRDPALDVPKFKVYLDQNDYSTAKGV 420
 DB 361 LEPSTLQNHNTAASSPLTFEIMSDDTPKGLAFRDPALDVPKFKVYLDQNDYSTAKGV 420
 OY 421 LGAGYQALMLARVLDGOALMLGLHMLVLEVDTCQOTLEVYRVLALYLGSSLGTERES 480
 DB 421 LGAGYQALMLARVLDGOALMLGLHMLVLEVDTCQOTLEVYRVLALYLGSSLGTERES 480
 OY 481 SSGGMPDVOERKATELRLQTLSEILSKCSHNVTETORSLSCEBELKNDQIHEDN 540
 DB 481 SSGGMPDVOERKATELRLQTLSEILSKCSHNVTETORSLSCEBELKNDQIHEDN 540
 OY 541 KSJOKIOCCDDKMHFTYKOKKSRMRPGLSYNEQOIKHKLKVNFSLAKRLVFOBEVY 600
 DB 541 KSJOKIOCCDDKMHFTYKOKKSRMRPGLSYNEQOIKHKLKVNFSLAKRLVFOBEVY 600
 OY 538 RSTQIOCCDDKMHFTYKOKKSRMRPGLSYNEQOIKHKLKVNFSLAKRLVFOBEVY 597
 DB 538 RSTQIOCCDDKMHFTYKOKKSRMRPGLSYNEQOIKHKLKVNFSLAKRLVFOBEVY 597
 OY 601 QTYOVSLVTHGKRMROYARQNLHLIGHSVATCNSEARGAOSLKNIPD---QLILDR 656
 DB 601 QTYOVSLVTHGKRMROYARQNLHLIGHSVATCNSEARGAOSLKNIPD---QLILDR 656
 OY 598 OKYQASLVTHGKRMROYARQNLHLIGHSVATCNSEARGAOSLKNIPD---QLILDR 657
 DB 598 OKYQASLVTHGKRMROYARQNLHLIGHSVATCNSEARGAOSLKNIPD---QLILDR 657
 OY 657 ASBGAIVSQPMAPHPGPRKQDLYFMQELCNDMKLLADIDNNMLIERLHVPSPAD 716
 DB 657 ASBGAIVSQPMAPHPGPRKQDLYFMQELCNDMKLLADIDNNMLIERLHVPSPAD 716
 OY 717 V 717
 DB 717 V 716

RESULT 3
 IKKB HUMAN STANDARD; PRT; 756 AA.
 ID 014920: 075327:
 AC 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (I-kappa-B-kinase beta) (IKKB) (IKB-beta) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 CN IKKB OR IKKBK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
 RC TISSUE=Cervical carcinoma;

RX MEDLINE=98008813; PubMed=9346484;
 RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
 RT NF-kappaB activation.";
 RL Science 278:860-866(1997).
 RN [12]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RX MEDLINE=98008814; PubMed=9346485;
 RA Moronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
 RT "IkappaB kinase-beta: NF-kappaB activation and complex formation with
 RT IkappaB kinase-alpha and NIK.";
 RL Science 278:866-869(1997).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=99032998; PubMed=9813230;
 RA Hu M.C.-T., Wang Y.-P.;
 RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RN [14]
 RP SEQUENCE FROM N.A., AND GENE MAPPING.
 RX MEDLINE=98438415; PubMed=9763654;
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
 RT "Assignment of IkappaB kinase beta (IKKB) to human chromosome band
 RT 8p12-3p11 by in situ hybridization.";
 RL Cytogenet. Cell Genet. 82:32-33(1998).
 RN [15]
 RP SEQUENCE OF 1-256 FROM N.A.
 RC TISSUE=Lung;
 RX Strausberg R.;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [17]
 RP REVIEW.
 RX MEDLINE=20178139; PubMed=10712233;
 RA Uebachs C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of
 RT mucosal inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, PLACENTA, SKELETAL
 CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, TESTIS AND
 CC PERIPHERAL BLOOD.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
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DR EMBL: AF029684; AAC51860.1; -
 DR EMBL: AF080158; AAD08997.1; -
 DR EMBL: AF031416; AAC64675.1; -
 DR EMBL: BC006231; AAH06231.1; -
 DR MIM: 603258; -
 DR InterPro: IPR000719; Euk_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; kinase; 1.
 DR Pfam: PF00240; ubiquitin; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKc_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
 KW phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).
 FT NP_BIND 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 177 177 PHOSPHORYLATION.
 FT MOD_RES 181 181 PHOSPHORYLATION.
 FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO EFFECT ON BINDING TO NIK.
 FT MUTAGEN 177 177 S->A: DECREASE OF ACTIVITY.
 FT MUTAGEN 177 177 S->E: FULL ACTIVATION.
 FT MUTAGEN 181 181 S->E: DECREASE OF ACTIVITY.
 FT CONFLICT 231 256 WSKVRSKSEVDIVSDDLQVYKFS -> CYRMPSTVAH SCNSVTLGGKRGKMTS (IN REF. 5).
 FT CONFLICT 425 425 Q -> H (IN REF. 1).
 FT SEQUENCE 756 AA; 86563 MW; F9CAD671AE9E14E CRC64;
 Query Match 11.7%; Score 437.5; DB 1; Length 756;
 Best Local Similarity 23.5%; Pred. No. 8.2e-21;
 Matches 187; Conservative 118; Mismatches 308; Indels 183; Gaps 27;
 QY 9 WHTDLLGQATASYKRNKSGGVVAVKFNSSAYRPREVQVREVEVRLRNHONIV 68
 DB 15 WEMERLGTGFGVNIIRHNDTEGQAIKCCROELSPRNERMCLEQIMRLTHENV 74
 QY 69 KLFAYEE---TGSRKQVILMEYCSSGSLVLEDEPTEFGISEEFLVLRGVAGNM 124
 DB 75 AARDVPEGMQMLAPNDLPRLAMEYCGGDLRKYLNOFENCGLREGALITLLSDIASLR 134
 QY 125 HLRNGIYHRDIKPGNIMRLVGEESGSIYKLSDCGARKLDDDEKFSVYGTETYLHPDM 184
 DB 135 YLHNRIRIHRRLKENVIVLQGGED-RLIHKIIDIGYAKELDQSGSLTSFVGTLYLAPEL 193
 QY 185 YERAVLRKPOQKAGVTVLMSISGVTLYHATGSLPIFPFGP-----RRNKEMIRY 237
 DB 194 LE-----QOKYTVIVDWSFGTLAFECITGRPLRMQRPVQWMSKRSKRVSEVIV 245
 QY 238 TTEKPAAGISTQKQENGPLEMSYLPITRGLSKGLONOLVPIIANIL-----EVERDKC 292
 DB 246 SEDL-----NGTVKFSSSLPYRNNSLVLERLEKMLQMLAMHPRQGTDP 293
 QY 293 WGFDFEAFETSDILQRTIVIVFSLPQAVLHNVYIHAHNTAIFLEAVYEDTNTYPRKQRY 352
 DB 294 YGPRGCKKALDDILNKLVLHNLNVGTITHTYVTEDESLOSISKARIQDQGTIPREDOEL 353
 QY 353 LFESHPVLEPSLSAQIIA-----HTAASSPLTFESMSDTPKGLAFRDPALDVPRKY 405
 DB 354 LOEAGLALIDPKPATQCSIGKINEGHTLMDLVFLFDSNKIYEVQISRPQ---PEVS 410
 QY 406 -----PKVLQADYSTAKVLAGAGVQALMLAVLLDQALMRGLHW-VLEVLQDTCCQ 458
 DB 411 SCLIQEPKRLV-AFPOLR-----VW-----GOVWHSIQTLTKEDCNR 446

QY 459 TLEVTALIVL---GSSLGERESSGGMADV----- 488
 DB 447 LQOQGRAMMILRNNSCLSKKNSMASMSQQLAKLIDFETTSIQIDLEKYSDETCIT 506
 QY 489 -----QERKEATEL---RTRQTLSEILSKSHVTEFORS-----LSCIGEE 528
 DB 507 SDKLLANRMEQAVELCGRENEVKLLVERMALQTDIVDQSPMRKOGGTDLDEQ 566
 QY 529 LL-----KNRQIHEDNKS-----IKRIQCCILKMHPIYQFKSMRGLSYNE 574
 DB 567 ARELYRLREKPRQGRREGDSQEVNRLLOAIQSEKVKVITYQLSKT-----VCKQK 621
 QY 575 QIHLDKYNESHAKRLLOVFOEECVOTYOVSLVTHGR--MRQVRAQNLH-LIGHSV 631
 DB 622 ALLELPKV-----EEV-----VSLMNEDEKTVVRLQEKRKELNMLLKIA 662
 QY 632 ATCNSEARQAQESLNTKIFDQLLDLRASEQAEVSPQMA-----PHRPDPKLVFHKQEL 687
 DB 663 SKVGPVSGSPDSMN-----ASRLSQPOLMSQSPSTASNSLPEPAKSEELVAENHL 715
 QY 688 CNDKLLAFDLODNMR 703
 DB 716 CT---LLENALQDTVR 728
 RESULT 4
 IKKB_MOUSE STANDARD; PRT; 757 AA.
 AC 088351; Q9RLJ6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (I-kappa-B kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIB).
 GN IKKB OR IKKBK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
 RC STRAIN=C57BL/6; TISSUE=Spleen;
 RX MEDLINE=98188238; PubMed=9520401;
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
 RT Okumura K.;
 RT "Differential regulation of IkappaB kinase alpha and beta by two
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
 RT protein kinase/ERK kinase-1";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that
 RT constitutively phosphorylates serine residues of Ikb.";
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP DEVELOPMENTAL STAGE.
 RX MEDLINE=99455228; PubMed=10523828;
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
 RT pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
 RT developmentally regulated protein kinase.";
 RL Oncogene 18:5514-5524(1999).
 RN [4]
 RP IKK PHOSPHORYLATION.
 RX MEDLINE=99038238; PubMed=9819420;
 RA Nemoto S., DiDonato J.A., Lin A.;
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein
 RT kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [5]

RP REVIEW.
 RX MEDLINE-20178139; PubMed-10712233;
 RA Jobin C., Sartor R.B.;
 RT "The IkappaB/NF-kappaB system: a key determinant of mucosal
 inflammation and protection.";
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MEK1, MAPK14/NIK, IKAP AND IKK-ALPHA-P55-P50
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE
 CC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: WHILE IT IS EXPRESSED UBICUOUSLY THROUGHOUT
 CC THE MOUSE EMBRYO, AT E9.5 DAY ITS EXPRESSION BEGINS TO BE
 CC LOCALIZED TO THE BRAIN, NEURAL GANGLIA, NEURAL TUBE, AND IN LIVER
 CC AT E12.5 DAY. AT E15.5 DAY, THE EXPRESSION IS FURTHER RESTRICTED
 CC TO SPECIFIC TISSUES OF THE EMBRYO.
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAPK14/NIK.
 CC WEAKLY AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPPAB KINASE SUBFAMILY.
 CC -----
 CC THE SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF026524; AAC23557.1; -;
 DR EMBL: AF088810; AAD52095.1; -;
 DR MGD: MGI:1338071; Ikbb.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE.NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 15 300 PROTEIN KINASE.
 FT DOMAIN 458 479 LECTICINE-ZIPPER (POTENTIAL).
 FT DOMAIN 737 742 NEMO-BINDING.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 145 145 BY SIMILARITY.
 FT MOD_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 56 56 N -> D (IN REF. 2).
 FT CONFLICT 343 343 N -> D (IN REF. 2).
 FT CONFLICT 356 356 L -> E (IN REF. 2).
 FT CONFLICT 390 390 L -> F (IN REF. 2).
 FT CONFLICT 406 406 P -> Q (IN REF. 2).
 FT CONFLICT 573 573 K -> R (IN REF. 2).
 FT CONFLICT 736 757 TLDSWLMQMEDERCSLEQDQCD -> VTA (IN REF.
 FT 2).
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;

Db 15 WEKEREITGEGFNVIRHMHNOATGEQIAIK--OCROELSPKRNRRKCLEIQIMRLNHP 71
 Qy 66 NIVKLFVAEE---TGSGROKVLIMEYCSGSLSLVEDPENTFGLSEEPVLVRCVYA 121
 Db 72 NVVAARDVEGQONLAPNDLPILAMEYOGGDLRRYVLMQFENCGLRGAVLCILSDIAS 131
 Qy 122 GNNHLRENGIVHRDIPGNIIMRLVEBEGOSYKLSDFGAARKLDDKDFVSYGTETLH 181
 Db 132 ALRYLHKNRILHRDLKPNENIVLOQGEK-RLHKIIDLGAKELDQSLCTSPVGLQVYA 190
 Qy 182 PMYERAVLRKQQAQAFQVTDMSIGVLYHAATGSLPFIPEGP-----RNRKEIM 234
 Db 191 PELLE-----QKRYTYVDMWSFGTLAEFCITGFREFLPMQPVOMHSKVRQKSEVD 242
 Qy 235 YRTTEKPAIGASIGOKOENGPLEMSYSLPTICRLSMGLONLVPLANIL-----EYEE 289
 Db 243 IYVSEDL-----NGAVKFSLSLPFPNNLSVAERLEKMIQLMLMNHPRQGT 290
 Qy 290 DKCWGFDFPFAETSDILORTVIVHESLPQAVLHVYIHAHTIAFLVAVYEQVNTPRH 349
 Db 291 DPQYGNCFRMLDIDLNLKLVLMVMTGVHTVPVTEDESLOSLKTRIQENTGILETD 350
 Qy 350 QETLPEGHCVLEPRLSNQIHNTAASPLTL-----FSMSD-----TPKGLAFRD 396
 Db 351 IELLQAGLVLLPDKPATQCIDSKTNEGTLTDMDLVFLDSKINYEQTTP-----RP 405
 Qy 397 PALDVEFVPKYDLQADYSTAGVLGAGYQALMLARVLLDGOALMLRGLHWJEVLDPYC 456
 Db 406 PEPVSVCILQEFKRNLSFFQLRWG---QYWH-----IQTLKECC 444
 Qy 457 QQTLEVTFRALLYL---GSSLGTER-----FSSGGMPOVERKENTE-- 496
 Db 445 NRLOQOQRAAMMSLLNNNSCLSKMKMASTAQOLKAKLDLFFRTSLDIDLEKTKQTEFG 504
 Qy 497 -----LRTRLQTLSEILSCSH-----NVTETORS-----LSCIG 526
 Db 505 ITSDKLLLAHREKQAVEQCGRENQVKKHLVERMALQDTIVDLQSRPMKRGGLDDE 564
 Qy 527 EELL-----KNRQIHEDNKS-----IKIQCLDMKMHFYKQFKSRMRPLSYN 572
 Db 565 EQARELYRKLRKRPQDRTGDSQEWRLRLQAIQSFKKRVLYIQLSKT-----VYCK 619
 Qy 573 EEOIHLKLVNFSHLAKRLQVTOECVOTYQVSLVTHGR--MRVQAQNHIL-HLIGH 629
 Db 620 QKALELPPRV-----EEV-----VSLNDEDERVYRLQERKQKELMNLKTI 660
 Qy 630 SVATCNSEARGAQESLNKIFDOLLDRASQGAESVPOPM-----PHGPPKDLVFM 684
 Db 661 ACSKVNGPVSGSPDSMN-----VRLSHPG-QLMSPSSACDSLPESDKSEELVAA 712
 Qy 685 QELCNMDKLLAPDLQD 700
 Db 713 HALCSRLSEA---LQD 725
 RESULT 5
 ID IKRB_RAT STANDARD; PRT; 757 AA.
 AC 090Y78;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
 DE (1-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase beta)
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).
 GN IKKB OR IKKBK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 ZHANG Y., SUN S., RAYLD K.;

ID	IKKA_MOUSE	STANDARD:	PRT:	745 AA.
AC	060680; Q9D2X3;			
AD	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Inhibitor of nuclear factor kappa-B kinase subunit (EC 2.7.1.-)			
DE	(I-kappa-B kinase alpha) (IKKA) (IKK-alpha) (I-kappa-B kinase)			
DE	(I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitons			
DE	kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).			
GN	IKKA OR CHUK			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	STRAIN=BALB/c;			
TX	MEDLINE=96044444; PubMed=7558004;			
TX	Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.,			
TX	"CHUK, a conserved helix-loop-helix ubiquitons kinase, maps to human			

RT chromosome 10 and mouse chromosome 19.";
RN Genomics 27:348-351(1995).
RN [12]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN-BALB/c;
RX MEDLINE=965258427; PubMed=8777433;
RA Connolly M.A., Marcu K.B.;
RT "CtHd, a new member of the helix-loop-helix and leucine zipper
RT families of interacting proteins, contains a serine-threonine kinase
RT catalytic domain.";
RL Cell. Mol. Biol. Res. 41:537-549(1996).
RN [13]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC STRAIN-C57BL/6J; TISSUE-Colon;
RX MEDLINE=11085660; PubMed=11217851;
RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kikuta K., Matsuda H., Ashburner M., Batilov S., Casavant T.,
RA Pletschmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Knehl P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Stablil F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Grossstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gunsberg S., Hill D., Hoffman M., Hume D.A., Kamlay M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima T., Mazzarelli T., Komhaeys P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata S., Storch K.-F.,
RA Suzuki H., Toyokake K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsuke S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [14]
RP ALTERNATIVE SPLICING.
RX MEDLINE=20198447; PubMed=10733566;
RA McGenzie F.R., Connolly M.A., Balzarano D., Mueller C.R.,
RA Glezinas R., Marcu K.B.;
RT "Functional isoforms of Ikappab kinase alpha (IKKalpha) lacking
RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and
RT IKKbeta have different activation requirements.";
RL Mol. Cell. Biol. 20:2635-2649(2000).
RN [15]
RP PHOSPHORYLATION BY MAP3K14/NIK.
RX MEDLINE=98188238; PubMed=9520401;
RA Okamura H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA Nakamura K.;
RT "Differential regulation of Ikappab kinase alpha and beta by two
RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT protein kinase/ERK kinase-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN [16]
RP IKKA-IKKB BINDING.
RX MEDLINE=99212141; PubMed=10195894;
RA Delhase M., Hayakawa M., Chen Y., Karin M.;
RT "Positive and negative regulation of Ikappab kinase activity through
RT IKKbeta subunit phosphorylation.";
RL Science 284:309-313(1999).
RN [17]
RP IKK PHOSPHORYLATION.
RX MEDLINE=99038238; PubMed=9819420;
RA Nemoto S., Didonato J.A., Lin A.;
RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein
RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL Mol. Cell. Biol. 18:7336-7343(1998).
RN [18]
RP REVIEW.
RX MEDLINE=20178139; PubMed=10712233;
RA Jobin C., Sartor R.B.;
RT "The I kappa B/NF-kappa B system: a key determinant of
RT mucosal inflammation and protection.";

[illegible]

Db 75 KACDVEELNFIINDVPLAMEYCSGGDLRLKLNKPCNCGILKESQILSLSDIGSIRY 134
 QY 126 LRENGIVHHDIKRGNIMRLVGECCOSIYKLSFGARKIDDEKVEVSYGTEYLHPMY 185
 Db 135 LHEKTIHHDIAENIV-LQDVGGKTIHKTIDLGAKADDOGSICTSFVGTLYLAPELF 193
 QY 186 ERAVLKPKQAKAGVTVLMSIGVLYHAATGSLPFI--PFGGPRRNKEIMYRIITEK 241
 Db 194 E-----NKRYTATVDVWSECTWFECTIAGYRPLHHLQPFTHKEIK-----KK 237
 QY 242 PAGALSTQKONGPLEMSYSP---IICRLSMGLONOLVPLAN-----ILEVE 288
 Db 238 DKRCIFACEEM-TGEVRRSSHLPQNSICSLVEEMESMLQIMLWMDPOQRGPIDLTK 296
 QY 289 EDKCGFDPQFAETSDILQRYIVHVSFLPOAVLHHVYIHAHTIATFLAAYVQOTNVPK 348
 Db 297 QPRC-----PALMDHILNLKIVHILNMTSAKIIISFLPDCDSLSIOSRIEREIGITWG 350
 QY 349 HOEYLF-----GHPCVLEPSLSNQHIT-----AMTASSPPLTFSMSDTPKG 391
 Db 351 SEELLSEGTISLDPRKPAQCVLDGVRGDSYMYVYLFDPKSTYVEGPPASRSLSDCV--N 408
 QY 392 LAFRPDLDPK-FVPKV-----DLQADYSTAKVGLAGVQALMLAVLDDQALM 441
 Db 409 YIVODSKTQLPRIOLKRYMAEAVHYVSGLKEDYSR---LFGQRAAMLS--LRYNML 462
 QY 442 LRGLHWLEVLQDTCQOQLEVTALTYLIGSSLGTERFSSGS--GMPDVORKEATELRT 499
 Db 463 TKMKWTLLISASQO-LKAKLEFFRKSII-----QLDEREYSEQMTYGISSEKMLKMKMEE 516
 QY 500 RQGTISEI-----LSKSHNTEYORS-----LSCLQEBEL-----LKNR- 533
 Db 517 KAIRHSEGVIGYLEDQIMSLHTEIMELQKSPYGRQGLMESLEQRAIDLYKOLKHPRP 576
 QY 534 DOIHEDNKSIQKIOCCLDKMHPIYKQEFKSRMRPGLSYNEQIHKLPKVNESHAKRL- 591
 Db 577 DLYSDSTEWKII-----IVHTVQSQ-----DVALKEFLGHSLKGLCC 614
 QY 592 -----LQVROECVQYQVSLVTHGRMRQVORAQNHLLIGHSVATCNSERGA 641
 Db 615 KOKIIDLPRKEVALSNKEADNTVMFGKROKEI-----WHLL-KIACQSSASRL 666
 QY 642 QES-----LNKIFQDLDRASQGAQVSPQAPAPHPGPKDLVFMQCLCDMK 692
 Db 667 VGSSEGVTPPVSAWMLPPTLADREHPLTCVTPQ-----DGETLAQMIENINCLG 718
 QY 693 LLAFLDLDNN 702
 Db 719 HLSTIIRKAN 728

RESULT 7
 IKKA_HUMAN
 AC 015111: 014666; 013132; 092467;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
 DE (I kappa-B kinase alpha) (IKBKA) (IKK-A) (Ikkappa kinase)
 DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitons
 DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKB1KA).
 GN IKKA OR CHUK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
 RC TISSUE=T-cell;
 RA MEDLINE=97386461; PubMed=9244310;
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
 RT "Identification and characterization of an Ikkappa kinase.";
 RT

RL Cell 90:373-383(1997).
 RN [2]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP MEDLINE=97394468; PubMed=9252186;
 RX Didonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
 RT "A cytokine-responsive Ikkappa kinase that activates the transcription
 RT factor NF-kappaB".
 RN Nature 388:548-554(1997).
 RN [3]
 RN SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
 RP SER-176.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=98008813; PubMed=9346484;
 RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
 RT "IKK-1 and IKK-2: cytokine-activated Ikkappa kinases essential for
 RT NF-kappaB activation".
 RL Science 278:860-866(1997).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Heart;
 RC MEDLINE=99032998; PubMed=9813230;
 RX Hu M.C.-P., Wang Y.-P.;
 RT "Ikkappa kinase-alpha and -beta genes are coexpressed in adult and
 RT embryonic tissues but localized to different human chromosomes.";
 RL Gene 222:31-40(1998).
 RN [5]
 RN SEQUENCE OF 32-745 FROM N.A.
 RP TISSUE=Cervical carcinoma;
 RX MEDLINE=96258427; PubMed=8777433;
 RA Connelly M.A., Marcu K.B.;
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper
 RT families of interacting proteins, contains a serine-threonine kinase
 RT catalytic domain".
 RL Cell. Mol. Biol. Res. 41:537-549(1995).
 RN [6]
 RN PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF S-176; T-179 AND
 RP S-180.
 RX MEDLINE=98188283; PubMed=9520446;
 RA Ling L., Cao Z., Goeddel D.V.;
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
 RT Ser-176".
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
 RN [7]
 RN PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
 RP MEDLINE=99413720; PubMed=10485710;
 RX Ozes O.N., Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M.,
 RA Donner D.B.;
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt
 RT serine-threonine kinase.";
 RL Nature 401:82-85(1999).
 RN [8]
 RN IKKA-IKKB BINDING.
 RP MEDLINE=99212141; PubMed=10195894;
 RX Delinas M., Hayakawa M., Chen Y., Karin M.;
 RT "Positive and negative regulation of Ikkappa kinase activity through
 RT IKKbeta subunit phosphorylation".
 RL Science 284:309-313(1999).
 RN [9]
 RN IKK PHOSPHORYLATION.
 RP MEDLINE=99038238; PubMed=9819420;
 RX Nemoto S., Didonato J.A., Lin A.;
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
 RL Mol. Cell. Biol. 18:7336-7343(1998).
 RN [10]
 RN REVIEW.
 RP MEDLINE=20178139; PubMed=10712233;
 RA Jobin C., Sartor R.B.;
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal
 RT inflammation and protection".
 RL Am. J. Physiol. 278:C451-C462(2000).
 CC -I- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO

CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
 CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED
 CC WHEN DEPHOSPHORYLATED.
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT
 CC ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
 CC ALSO BIND TO MAPK14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50
 CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- PTM: PHOSPHORYLATED BY MAPK14/NIK, AKT AND TO A LESSER EXTENT BY
 CC MEK1, AND DEPHOSPHORYLATED BY PP2A, AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC IKAPAB KINASE SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AF012890; AAC51662.1; -
 CC EMBL: AF009225; AAC51671.1; -
 CC EMBL: AF080157; AAD08996.1; -
 CC EMBL: U22312; AAC50713.1; -
 CC HSP: P05132; IRIX.
 CC MIM: 600664; -
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR002290; Ser_thr_pkinase.
 CC Pfam: PF00069; pkinase; 1.
 CC PRINTS: PR00109; TYRKINASE.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase: Serine/threonine-protein kinase; ATP-binding;
 CC KW Phosphorylation.
 CC FT DOMAIN 15 302 PROTEIN KINASE.
 CC FT DOMAIN 455 476 LECITINE-21PPER (POTENTIAL).
 CC FT DOMAIN 738 743 NEMO-BINDING.
 CC FT NP_BIND 21 29 ATP (BY SIMILARITY).
 CC FT BINDING 44 44 ATP (BY SIMILARITY).
 CC FT ACT_SITE 144 144 BY SIMILARITY.
 CC FT MOD_RES 23 23 PHOSPHORYLATION (BY AKT).
 CC FT MOD_RES 176 176 PHOSPHORYLATION (BY MAPK14).
 CC FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND
 CC FT MUTAGEN 44 44 DECREASE OF KINASE ACTIVITY.
 CC FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.
 CC FT MUTAGEN 176 176 K->M: LOSS OF AUTOPHOSPHORYLATION.
 CC FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF
 CC ACTIVITY.
 CC FT MUTAGEN 176 176 S->E: FULL ACTIVATION.
 CC FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.
 CC FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.
 CC FT CONFLICT 543 543 E -> G (IN REF. 2).
 CC FT CONFLICT 604 604 L -> R (IN REF. 5).
 CC FT CONFLICT 679 680 TS -> AY (IN REF. 5).
 CC FT CONFLICT 684 684 P -> A (IN REF. 3 AND 5).
 CC FT CONFLICT 686 687 TS -> DL (IN REF. 5).
 CC FT SEQUENCE 745 AA; 84653 MW; 7A9059BC98A56C2 CRC64;
 OY 9.5%; Score 352.5; DB 1; Length 745;
 Best Local Similarity 22.6%; Pred. No. 2,4e-15;
 Matches 170; Conservative 114; Mismatches 292; Indels 177; Gaps 33;
 OY 9 WHTDILGGATASYTKARKNKSGEYVAVVKFNSATYRPREVOYREVEVLRNRHNIYV 68
 DB 15 WEMREHLAGGFGVNCVLYOHRELDKIAIKSCRELSTKNEERMCHEQIOMKLNHANV 74
 OY 69 KLFVAVERTGSGROKVLII-----MEYCSGSLSLVLDPRNFTGLSEEFELVLRGVYA 121

DB 75 KACDVE-----ELNLIHIDVPLAMEYCSGDLRLKLNKPCNCCGKLSQILSLSDIGS 130
 OY 122 GANHLENGVHNDITPRGIMILYGEESGYIKSLDFGAARLDDDEKVFVSYYGTEETH 181
 DB 131 GYRLEHKNKIKHIDKPEINV-LQDVGKTIHKIIDLGAQYVDGSLCTSVGLQIOLA 189
 OY 182 PDYERAVLRKPKPOAKAFVYVLDMSIGVTLVHAATGSLPFI-----PFGGPRNKEIMYRI 237
 DB 190 PELFE-----NKPYTATVDVMSFGTWPEEINGRFLHLPFTWHEKIK----- 235
 OY 238 TTEKPAISGTOKQENGLPMSYSLP---ITCRLSMGIQNDLVPLAN-----I 284
 DB 236 --KKDPKIFACEEM-SGEVRFSSHLPPNLSLCLVPEEMWLDLMLWDPQGRGPDV 292
 OY 285 LEVEDKCMWGFQPFATSDILOFVIVHESLPQVLIHVYIHAHTTIAIFLEAVYEQTN 344
 DB 293 LTLKQPRC-----FVLMHILMLKIVHILNMTSAKIFLPPDSLSLSQRIERETG 346
 OY 345 VTPKHQVLEFE-----GHPVLEPSLSAQHI-----AHTAASPPLTFLSMSSD 387
 DB 347 INTSGQLSETGISLDPKRPASQVLDGVRGCDSYMYVLFDSKTYEGPFPASRSLSDC 406
 OY 388 TPKGLARDPALDVPK-VPKV-----DQADYSTAKVGLGAGYQALMARVLDG 437
 DB 407 V-VYIVODSKIQLPILQLRKVAEAVHYVSGLKEDYSR-----LFG 447
 OY 438 Q-ALMLRGLHW-VLEVLDPTCOOTLEVTRTALLYGSS--LGTERRSSGMPDQERK 492
 DB 448 QRAMLSLRNNAULTKMTNLTLSASQOLKAKLEFFPKRSIQDLERYS-----EQMT 499
 OY 493 EATELRRLQTLSEILSKSHNTETORSLSCEBELKRRDIIHEDNKS-----I 543
 DB 500 YGISSEKMLKMKMEKKAHYA--EVGVIGYLEDQIMSLHABIMELQSPYGRROGDLM 557
 OY 544 OKI-OCCLDKMHPFYKQFKSRMPG-LSYNEED-----IKKLD-----KYNFSLAK 589
 DB 558 ESLERPID--LYKQLK--RPSDHSYSDSEMYKIIVHYVQSDRYLKLFLHLK 610
 OY 590 RL-----LOVFECEVQTYOVSLVTHGKRMROYORANHLHLIGHSVATFNCSE 637
 DB 611 LLGCKQKTIIDLPVKEVALSNIKREADVTVMQGRKEI-----WHL-LKIACQSS 662
 OY 638 ARGADSELNKLPDQULLDRASEGAEVSPQMA 670
 DB 663 AAS-----LVGSSLEGA-VTPQTS 681
 RESULT 8
 ID ULK1_MOUSE STANDARD: PRT: 1051 AA.
 AC 070405;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase ULK1 (EC 2.7.1.1-) (unc-51-like kinase
 1) (unc51.1 serine/threonine kinase).
 GN ULK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98262945; PubMed=9600096;
 RA Yan J., Kuroyanagi H., Kuroiwa A., Matsuda Y., Tokumitsu H.,
 RA Tomoda T., Shirasawa T., Muramatsu M.-A.;
 RT Identification of mouse ULK1, a novel protein kinase structurally
 related to C. elegans UNC-51*;
 RL Biochem. Biophys. Res. Commun. 246:222-227(1998).
 RN [2]
 RP SEQUENCE FROM N.A.

Query Match	8.0%;	Score 299.5;	DB 1;	Length 1051;
Best Local Similarity	24.2%;	Pred. No. 9.8e-12;		
Matches 108; Conservative	60;	Mismatches 148;	Indels 131;	Gaps 14;

[illegible]

Db 351 SCDTDDFWMPAGPFG-DLVAEAAASAK 376

RESULT 9

ID	UHL1_HUMAN	STANDARD;	PRT; 1050 AA.
AC	075385;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Serine/threonine-protein kinase UHL1 (EC 2.7.1.-) (Unc-51-like kinase 1).		
DE	UHL1.		
GN	UHL1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98360094; PubMed=9693035;		
RA	Kuroyanagi H., Yan J., Seki N., Yamanouchi Y., Suzuki Y.-I.,		
RA	Takano T., Muramatsu M.-A., Shirasawa T.;		
RT	"Human UHL1, a novel serine/threonine kinase related to UNC-51 kinase		
RT	of <i>Caenorhabditis elegans</i> : cDNA cloning, expression, and chromosomal		
RT	assignment.";		
RL	Genomics 51:76-85(1998).		
CC	-1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED. DETECTED IN THE		
CC	FOLLOWING ADULT TISSUES: SKELETAL MUSCLE, HEART, PANCREAS, BRAIN,		
CC	PLACENTA, LIVER, KIDNEY, AND LUNG.		
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	AP01/UNC-51/UHL1 SUBFAMILY.		
CC	-----		
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	CC	EMBL; AF045458; AAC3326.1;	-.
DR	HSSP; P00523; 2PTRK.		
DR	MIM: 603168:	-	
DR	InterPro; IPR000719;	Euk_pkinase.	
DR	InterPro; IPR002290;	Ser_thr_kinase.	
DR	InterPro; IPR001245;	Tyr_pkinase.	
DR	Pfam; PF00069;	pkinase; 1.	
DR	PRINTS; PR00109;	TYRKINASE.	
DR	SMART; SMO0220;	s_trc; 1.	
DR	PROSITE; PS00107;	PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS00108;	PROTEIN_KINASE_ST; 1.	
DR	PROSITE; PS50011;	PROTEIN_KINASE_DOM; 1.	
KW	Transferase; Serine/threonine-protein kinase; ATP-binding.		
FT	DOMAIN	16..278	ATP BINDING SITE
FT	NP_BIND	22..30	ATP (BY SIMILARITY).
FT	BINDING	46..46	ATP (BY SIMILARITY).
FT	ACT_SITE	138..138	BY SIMILARITY.
FT	DOMAIN	297..310	POLY-SER.
SQ	SEQUENCE	1050 AA; 112601 MW; 4ED9B94028E3C138 CRC64;	
<hr/>			
Query Match	Best Local Similarity	7.9%; Score 294.5; DB 1;	Length 1050;
Matches	86; Conservative	54; Mismatches 118; Indels	69; Gaps 10;
OY	13 DLGGGATAVYYKARKNKSGEV-VAVKVFNSASRRPEVOVRFEFYLRRLHONIKLF 71 : : : : : : : : : : : : : : : + + + + +		
Dd	20 DLIIGHAAVAAYFVGKRHRKHDLLEAVAKVCINKNKLAKSQTLIGRIKIIRLLKEI KHEYNIALY 79 + + + + +		
OY	72 AVEETGGSRKVVLIMEYCSSLVSLEDPEPTFGLSDEEFLLVLCRVAGMNHIRENGI 131 + + + + +		
Dd	80 DFQEMANS--VTLMVESCTCGDGLADYLTHAMNT---LTSEDITRFLQLGIAGMRLLSKGI 134 + + + + +		

QY 132 VHRDIKPGNIMRLVGEEO-----SI-YKLSDFGAAKRLDDDEKFEVSYGTEYLHPDMY 185
 FT BINDING 65 65 ATP (BY SIMILARITY).
 FT ACT SITE 157 157 BY SIMILARITY.
 SQ SEQUENCE 966 AA; 111992 MM; 7115EAC01032BF94 CRC64;

Db 135 IHHDLKPPONTL-LSNPGAPRANPNISIRVKIADGFAFYILOSMMATLTCSPRYMAPEVI 193
 QY 186 ERAVLRRPOOKAFGVTVDLMSIGVTLYHAATGSLPIPGGPRRNKEIMYRITTEKPA 245
 Db 194 -----MSQHYDGRADLMSIGTIYQCLTGKAF-----QASSPQDLRLFYEKNKTL 239
 QY 246 ISCTQKQENPLEMYSILPTICRLSMGLONOLVPIIANILEVEEDKCKGDFDFAETSDI 305
 Db 240 VPIPRETSAPLR-----QLLIALIQRNHKRMDPDEDF----- 273
 QY 306 LQRTVHVFSLPQAVLHHVYIHAHNTI 332
 Db 274 -----HHFPLDASPSV 284

RESULT 10
 STD_MOUSE STANDARD; PRT; 966 AA.
 ID SRT10_MOUSE
 AC 055096;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase 10 (EC 2.7.1.37) (Lymphocyte-oriented kinase).
 DE CN SK10 OR LOK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RA MEDLINE=97426413; PubMed=9278426;
 RA Kuramochi S., Moriguchi T., Kuida K., Endo J., Samba K., Nishida E., Karsan Yama H.;
 RT "LOK is a novel mouse STE20-like protein kinase that is expressed predominantly in lymphocytes.";
 RT J. Biol. Chem. 272:22679-22684(1997).
 RL -1- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND HISTONE H1A ON SERINE AND THREONINE RESIDUES.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS SUCH AS SPLEEN, THYMUS, AND BONE MARROW.
 CC -1- PPM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. STE20 SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: D89728; BAA24073.1; -
 CC HSSP: P24941; ICKP
 DR MGD: MGI:1099439; SK10.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
 KW Phosphorylation; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; Coiled coil.
 FT DOMAIN 36 294 PROTEIN KINASE.
 FT DOMAIN 588 936 COILED COIL (POTENTIAL).
 FT DOMAIN 749 883 GIN-RICH.

FT NP_BIND 42 50 ATP (BY SIMILARITY).
 FT BINDING 65 65 ATP (BY SIMILARITY).
 FT ACT SITE 157 157 BY SIMILARITY.
 SQ SEQUENCE 966 AA; 111992 MM; 7115EAC01032BF94 CRC64;

Query Match 7.7%; Score 288.5; DB 1; Length 966;
 Best Local Similarity 21.8%; Pred. No. 4.5e-11;
 Matches 186; Conservative 125; Mismatches 300; Indels 243; Gaps 38;

QY 6 NYLHHTDDLLGCGATSAVYKARKKKSGEVAVKVFASARYRPREQVAREFYRLRNHQ 65
 Db 33 NDWEIVGELGDAGFGKRVYKAKKKGALAAAVETKS-EEBLEIYIEILITCDHP 91
 QY 66 NYKLVAVEETGSGRQKVLIM-EYCSGSLSYLEDPEPTFGISEEFLVLAACVAGNN 124
 Db 92 YIYKLLGAVYDS-KWIMTIEFCGAVDAIMELDR--GLTERQIQVVCROMLEALN 146
 QY 125 HLRNGIVHRDIKPGNI-MRLVGEQGSITYKLSDFG-AARKLDDDEKFEVSYGTEYLHP 182
 Db 147 FLHGKRIIHRDLKAGNVLMLEGD-----IRLADFGVSAKNLTKLRDSEFISTPYWMP 201
 QY 183 DMYERAVLRKPOOKA-FGVTVDLMSIGVTLYHAATGSLPIPGGPRRNKEIMYRITTEK 241
 Db 202 EV-----VLCETKDAIPYDIKADIMSIGITILEMAQIEPRHNL-NPMR--VLTKIAKSD 253
 QY 242 PAGAICTQKQENPLEMYSILPTICRLSMGLONOLVPIIANILE----- 286
 Db 254 PPTLIT-----PSKWSVEFRDFLKLALDKPETERPSAAOLHPFVSRYTSNKALRE 305
 QY 287 -VEEDKCKGDFDFAETSDILORTVHVFSLPQAVLHHVYIHAHNTIAIFLEAVEQTNV 345
 Db 306 LVAEAKAEVMEIEIDEGDEEDDAVD--AVPLVNH-----TDSANV 347
 QY 346 TPKEOXYLFEGHPCVLEPESLAQHIAHTAASPL-----TLFSMSDTP----- 389
 Db 348 T-----QPSIDSKNLLOD-SSTPLPSQPEPVNPGSPGSGGPIQTTSS 391
 QY 390 --KGLAFRDPALDP-----KVPVVDIADYATKAGVLGACYA 427
 Db 392 PADLSKNDNDLAKVPPLKSRPLSMARLQMDKEQIPDDENPSPASKSOKANOSRP 451
 QY 428 LMLARVLLDQALMLRLHNVLEVLQDTCCQTLTEVTATLLYIGSSIGT-EFSSSGSGM- 485
 Db 452 NSSALETLGGALTNGLLEPSSVTPSHSKRASC-----SNLSTESMDYGTSL 502
 QY 486 PDVERKEATEL-----RTR-----LQTLSELLSKSHNYETQ----- 519
 Db 503 ADLSLNKETSLSKSLHNTKLTTRRFVVDGEVYSITTSKIISDEKDEEMRLR 562
 QY 520 ---RSLSCGEEELKNRDQIHEDNKSIOKIQCCLDKNNFIYOKKSRMPCLSYNE-- 574
 Db 563 QELRELRLIQKEHRNDQOLS-----SKHELQLOMNH--KREOEIINAKKRYDVELE 613
 QY 575 -----QIHKLDKVNFSLKRLLOV-----FOECYQ----- 601
 Db 614 NLERQKQOVKMEODHSVRKKEKARRLEBODDYAKFOQLQOMKKEVSEVEKLPRQ 673
 QY 602 ---TYOVSIVTGRKRMQVOR---AQNHLILGHSVAT-----CNSEAKGAGSIN 646
 Db 674 QRKESMKQMEHSOKQRLDRDFAVAKQEDLELAKRLTTEENREICDKE---RDLCS 729
 QY 647 KIFDOLLIDRASDQAEVSPQPMARPHRPRDKDLYFHHQELCNMUKLAPL----- 698
 Db 730 K-KQELRLDR-----EALWEMEBHQLQERHOLV--KQQLKDOYFLQRLDLKKEKER 780
 QY 699 ---ODNRLIERL 708
 Db 781 EQMQRYNQRMMEQL 794

RESULT 11
 Y537_HUMAN

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ID Y537 HUMAN STANDARD: PRT; 661 AA.
AC 060285;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable serine/threonine-protein kinase KIAA0537 (EC 2.7.1.-).
GN KIAA0537.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ishikawa O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro."
RL CNA Res. 5:31-39(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AB011109; BAA25463.1;
DR HSSP: P00518; 1PKK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE_ST; 1.
KW Hypothetical protein; transferase; Serine/threonine-protein kinase;
KW ATP-binding.
FT DOMAIN 55 306 PROTEIN KINASE.
FT NP_BIND 61 69 ATP (BY SIMILARITY).
FT BINDING 84 84 ATP (BY SIMILARITY).
FT ACT_SITE 178 178 BY SIMILARITY.
SQ SEQUENCE 661 AA; 74304 MW; 806E37D52CA4718F CRC64;

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Query Match 7.7%; Score 285.5; DB 1; Length 661;
 Best Local Similarity 22.4%; Pred. No. 4.2e-11;
 Matches 151; Conservative 116; Mismatches 258; Indels 149; Gaps 32;

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QY 277 LVPILLANTLEVE-----EDKMGFDQFFAETSDIL--QRTYIHVSLPQAVLHH 323
DB 334 ESPLLARIIDMHRSTGLQADTEAKMKGLAK--PTTSEVMLEQR-----SLKSKKEN 375
QY 324 VYIHAHNTIAIFLEAVYEQTWTPKHQOEVLFECHP-CYLELSLSAONIAHTAA----- 375
DB 376 DFAQSGQ-----DAVPEPSKLSKSKPKKGLKKRSSEHRSHTGFEIGVG 422
QY 376 -SSPLTLFSSGSDPPKQ-LAFRDPALDVP-KFVPKYDLQADYSTAGVYL-----GAGY 425
DB 423 PALPST-FKMEQDLCTRGVLLPSSPEAEVPEKLSPK---QSATWPKKGLLKTQQRSGY 478
QY 426 QA---LMLARVLDLQGLMLRGLHWLEVLVDTOQQT---LEVTRLALYLGSSLGTERF 479
DB 479 YSSPERSSSSLSDNDVM--GSSIPSPSPDPARVTSHTSISCRKGIILKHS-----KY 531
QY 480 SSGSGMPDVORRKPATELRTQLTSELSSKSHNVEFORSLSCJGEELKKRRD----- 534
DB 532 SAGTMDFALVSPEMP-----LESLSEPGVPABEGLSRSPSSVSDSDVSSDSEDL 586
QY 535 QIHEDNKSIOQIQCCLDKMHEFYKQ-FKSGMRPGLSYNEEQIHKLDKVPFSLAKRLIQ 593
DB 587 DLOENRRARORIRSCVAENFLQIDFEGIQNRPQYLKRYNRRLADSEFSLTFD----- 642
QY 594 VFOECVQYQVSL 607
DB 643 --MDVYQVYKQAL 654

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RESULT 12
CC15 YEAST STANDARD: PRT; 974 AA.
AC P27636;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cell division control protein 15 (EC 2.7.1.-).
GN CDC15 OR YAR019C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92357012; PubMed=1495480;
RA Schweitzer B., Philippson P.;
RT "NPK1, a nonessential protein kinase gene in Saccharomyces cerevisiae
RT with similarity to Aspergillus nidulans nima."
RL Mol. Gen. Genet. 234:164-167(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=GRF88;
RX MEDLINE=91353080; PubMed=1882551;
RA Schweitzer B., Philippson P.;
RT "CDC15, an essential cell cycle gene in Saccharomyces cerevisiae,
RT encodes a protein kinase domain."
RL Yeast 7:265-273(1991).
RN [3]
RP REVISIONS TO 900-902.
RA Schweitzer B.;
RN Submitted (May-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RX MEDLINE=95028152; PubMed=7941740;
RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
RA Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
RT "Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
RT the 42 kbp SPOT-CENT-CDC15 region."
RL Yeast 10:535-541(1994).
RN [5]
RP SEQUENCE OF 865-974 FROM N.A.
RA Davies C.J., Hutchison C.A. III;

```

RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
 CC - FUNCTION: ESSENTIAL FOR LATE NUCLEAR DIVISION IN THE MITOTIC
 CC CYCLE. REQUIRED FOR INACTIVATION OF CDC2 KINASE ACTIVITY AT THE
 CC END OF MITOSIS.
 CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC - CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-4 IS THE INITIATOR.
 CC
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 CC or send an email to license@isb-sib.ch).

DR EMBL; X60549; CAA43041.1; -
 DR EMBL; X52683; CAA36906.1; -
 DR EMBL; L22015; AAC04965.1; ALT_SEQ.
 DR EMBL; M67445; AAA34400.1; -
 DR PIR; S15038; S15038.
 DR PIR; S25680; S25680.
 DR HSP; P11362; ITRK.
 DR SGD; S0000072; CDC15.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase.1.
 DR SMART; SM00220; S_TKC.1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM.1.
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
 DR Cell cycle; Cell division; Mitosis
 DR DOMAIN 25 272 PROTEIN KINASE.
 DR NP_BIND 31 39 ATP (BY SIMILARITY).
 DR BINDING 34 54 ATP (BY SIMILARITY).
 DR ACT_SITE 146 146 BY SIMILARITY.
 DR SEQUENCE 974 AA; 110352 MW; 7A69AB7FEE291991 CRC64;

Query Match 7.58; Score 278; DB 1; Length 974;
 Best Local Similarity 21.84; Pred. No. 2.1e-10;
 Matches 139; Conservative 101; Mismatches 216; Indels 182; Gaps 29;

QY 9 WHRDDLLGQATASVYKARKKSGEVAVVFNASASVRRPEVQ--VREVEVRLRNHON 66
 DB 25 YHLKVGIRSGYGVYKAIKHKDQVYAIR---EVTENDELDIAEISLTKNHNH 81
 QY 67 IVKLPVETGGSRQKVLINECSSGSLVLEDPENTFGISEEFLVLRVAVAGMHL 126
 DB 82 IVYHGFIRK--SYELYLILEYCANGSLRRLIS--RSTGLSENESTVYVOTLGLIKYL 137
 QY 127 RENGIVRDRKPGNIMLVGEEGOSIYKLSDFGARKLDDDEKVFVSYGEEVLRHPDME 186
 DB 138 HGGGVIRHROIKANIL---SADNIVYKLADPFCVSTVNSA--LTLAGLMMAPEDIL- 190
 QY 187 RAVLRKRPQAKAFVYVWDLMSIGVLYHAATGSLPFIPEGPRRNKEIMYRITTEKAPAI 246
 DB 191 -----GNRGASTLSDINSIGATVVEMLTKNPPY-----INHLT----- 223
 QY 247 SGTQKQENGLFEMSYSLPTICRLSMGLONOLVPLANI--LEVEEDKCMGCFDQFAETSDI 305
 DB 224 -----ANIYVAVENDTYPPSSPSEPLKDF 248
 QY 306 LQRTVI--HVFSLPQA--VLHHVYIHAHTIAI-----FLEAVY-----QTNV 345
 DB 249 LSKCFVKNNYKRTADOLKHWIINSTENKVKLKKFKEDFDADYHWDADFOEERLNI 308
 QY 346 TPKHQEYLFEGHPCV-----LEPSLSAQHIAHTAAS--PLT-----LFSMSDTPKG 391
 DB 309 SP--SKFSLRAAPVAENNQELDLPPTESQLSLQKSSSKRLTDLHLVFSVC----- 361
 QY 392 LARDDALDLPKVPKVDLQADVSTAKGVIGA-----GQALMLANVLLDQALMIRGLH 446

DB 362 --LENIAPIIECLSRITVYDKRLITAFGSIIFYVDQHNHSLRLKFIAMGSIPLITFEH 419
 QY 447 WLEVLDPTCOQTLEVRTALLYGSSIGTERSSGMPDQERKATELRRLQTLSE 506
 DB 420 LAKEFVIDPQTLIE---CGIMY-----PPNFAS-----LKPQKYLELVREFYDLS 464
 QY 507 ILSKSHNVETQSLSCIGELKNRDQIHEDK-----SIQK1-QCCLDK 552
 DB 465 TAFMCRMCFKHLDSL-----LNN--THERRAQSLKLKSLVAPWSEKILPLSDLS 515
 QY 553 MHFIYKQFKSRMRPGLSY-----NEQIHK 578
 DB 516 -----KLKKKILISQITVYVFKSINVMITNDQIKH 548

RESULT 13
 ID ST10_HUMAN STANDARD; PRT; 968 AA.
 AC 094804; 090TW4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase 10 (EC 2.7.1.37) (lymphocyte-oriented
 DE kinase).
 GN STK10 OR LOK.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99216434; PubMed=10199912;
 RA Kuramochi S., Matsuda Y., Okamoto M., Kitamura F., Yonekawa H.,
 RA Karasuyama H.,
 RT "Molecular cloning of the human gene STK10 encoding lymphocyte-
 RT oriented kinase, and comparative chromosomal mapping of the human,
 RT mouse, and rat homologues."
 RL Immunogenetics 49:369-375(1999).
 RN [2]
 RP SEQUENCE OF 814-968 FROM N.A.
 RC TISSUE-Testis.
 RA Bloeker H., Boecker M., Brandt P., Nemes H.-W., Gassenhuber J.,
 RA Wiemann S.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC - FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND
 CC HISTONE IIA ON SERINE AND THREONINE RESIDUES (BY SIMILARITY).
 CC - CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphorylated protein.
 CC - TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS.
 CC - PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
 CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC STE20 SUBFAMILY.
 CC
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DR EMBL; AB015718; BAA35073.1; -
 DR EMBL; AL133081; CAB61400.1; -
 DR HSP; P24941; IHCL.
 DR MIM; 603919; -
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase.1.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00220; S_TKC.1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM.1.

KW Transferase: Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation: Coiled coil.
 FT DOMAIN 36 294 PROTEIN KINASE.
 FT DOMAIN 573 947 COILED COIL (POTENTIAL).
 FT DOMAIN 750 884 GLN-RICH.
 FT NP_BIND 42 50 ATP (BY SIMILARITY).
 FT BINDING 65 65 ATP (BY SIMILARITY).
 FT ACN_SITE 157 157 BY SIMILARITY.
 SQ SEQUENCE 968 AA; 112134 MW; 15E245193EC553D CRC64;

Query Match 7.4%; Score 277; DB 1; Length 968;
 Best Local Similarity 22.1%; Pred. No. 2,5e-10;
 Matches 178; Conservative 118; Mismatches 284; Indels 224; Gaps 39;

QY 6 NYLMTDDLCOGATASYARKKSKGEVAVKVPNSASYRPPVQVREEVYLRILNHQ 65
 DB 33 NEWEIVGELDGAFGKVKAKNETGALAAKYETKS--EELEDYIVEIETLATCDHP 91
 QY 66 NIVKLFAYEETGSRQKYLIM-EKCSGSLSYLEDPEPTFGSLSEEFVLYLRGVAGMN 124
 DB 92 YIVKILGAYYHDG--KIMIMIEPCGAVDAIMEIDR--GLTERPQIQVYCRQMLEALN 146
 QY 125 HIRENGIYHRDIKPGNI-MRLVGEQSIYKLSDFG-AARKLDDKEFVSYYGTEEXLHP 182
 DB 147 FLHSKRILHRDLKAGNVMLTEGD-----IRLADFGYSAKMLKTLQKRDSEIGTPYMMAP 201
 QY 183 DMREAVYLRKQQAFCYTVLMSIGVLYLAAGSLPFIFPGGRNKEIMYITTEKP 242
 DB 202 EV--VMEETMKDPRDYKADLWSLGLTLEMAQIEPHNEL-NEMR--VLKINASDP 254
 QY 243 AGAISTGKOENGPLEMSYSLPTCRLSMGLONOLVPTIANIL----- 285
 DB 255 PILLT-----PSKMSVEPRDFIKALDKNPEPRSAQDLHPVSSITSMKALREL 306
 QY 286 -----EYEDKCKGFDQFAETSDILQRYIHVSLPQAVLHVYIHAHTIAIF 335
 DB 307 VAEAKAEVMEIEIDRDEEDDAVDASTLEN-----HTONS----- 344
 QY 336 LEAVAEQNVNPPKHOEYLFEGHPVLESLNIAHTAASPLTLFMSMDT----- 388
 DB 345 -----SEVSP-----PSLNADKPLESPSPFLAP--SQSQDSVNEPSSQ 381
 QY 389 PKG---LAERDP-----ALDVP--KEVP-KVDLQADYSTAKGYLAGYQALMLA 431
 DB 382 PGDRSLQTTSPVYVAPGNENGLAVPPLKRSRPVSMARIQVAQEKQVAEGGDLSPAA 441
 QY 432 RILLGQALMLGLMWLEVL--QDTCCQTL-----VTRTALLYL 470
 DB 442 N--RSQKASQSRPNSSALETTLGGEKLANGLSPRAQAAPGPKRSDSCSLCTSESMDY- 498
 QY 471 GSSLGTE-RFSSGSGMPDQERR--EATELTR-----LQTLSELISCKSHNVET 518
 DB 499 GNLSTDLNKNEMGSLSTKDPKIKYKTKRKRFVNVGVEVSIITSKISDEKDEDM 558
 QY 519 Q-----RSLSCGEBELIKNRDQIHEDNKSIOKIQCCIDKKNHGYTKO---FKKSRMRPG 568
 DB 559 RFLRQELRELRLQKEERHNOTLS-----NKHEDLEQMKRPFEDINAKKKEPFDE 612
 QY 569 L-SYNEDQIHKLIDKVFSLAKRLLOVROECVQTYQVSLYVNGRMVQV-----RAON 622
 DB 613 LEHLERQKQOQVEKEDDAVRR--REE-----ARRIRLEQDRDYTRQDE 655
 QY 623 HLHLIGHSAVTCNSEARGAQSINKIFDQLLDLRASQGAQVSPQMAHPNRPD--PRD 679
 DB 656 QLKIM-----KKEVKNNEVKLPR-----QQKESMKQKMEHNTQKKDLLRD 697
 QY 680 LVFHMQLCNMCKLAFDLQDNMR 703
 DB 698 EVAKQKE---DEIEMKRLTIDNR 718
 RESULT 14

CC7_SCHPO
 ID CC7_SCHPO STANDARD: PRT: 1062 AA.
 AC P41892;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cell division control protein 7 (EC 2.7.1.1).
 GN CDC7 OR SPBC21.06c.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RC MEDLINE=94313982; PubMed=8039497;
 RX Fankhauser C., Shtanus V.;
 RA "The cdc7 protein kinase is a dosage dependent regulator of septum
 RT formation in fission yeast.";
 RL EMBO J. 13:3011-3019(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Saunders D., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROTEIN KINASE ESSENTIAL FOR CELL DIVISION. PLAYS A
 CC KEY ROLE IN INITIATION OF SEPTUM FORMATION AND CYTOKINESIS. SEEMS
 CC TO INTERACT WITH CDC11.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC
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 CC or send an email to license@isb-sdb.ch).
 CC
 CC EMBL: X78799; CAA5382.1; -
 CC DR EMBL: AL035537; CAB36886.1; -
 CC DR HSSP: P11362; 1FGK
 CC DR InterPro: IPR000719; Euk_Pkinase.
 CC DR InterPro: IPR002290; Ser_Thr_Pkinase.
 CC DR Pfam: PF00069; Pkinase; 1.
 CC DR SMART: SM00220; S_TKc; 1.
 CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC KW Transferase: Serine/threonine-protein kinase; ATP-binding;
 CC Cell cycle; Cell division.
 KW DOMAIN 9 259 PROTEIN KINASE.
 FT NP_BIND 15 23 ATP (BY SIMILARITY).
 FT BINDING 38 38 ATP (BY SIMILARITY).
 FT ACN_SITE 131 131 BY SIMILARITY.
 FT DOMAIN 483 490 ASP/GDU-RICH (ACIDIC).
 SQ SEQUENCE 1062 AA; 119291 MW; 04459AD60C0E2EDD CRC64;

Query Match 7.4%; Score 276; DB 1; Length 1062;
 Best Local Similarity 26.3%; Pred. No. 3,2e-10;
 Matches 103; Conservative 64; Mismatches 130; Indels 94; Gaps 16;

QY 13 DLLGOGATASYARKKSKGEVAV-KVNSASYRPPVQVREEVYLRILNHQIVKLF 71
 DB 13 DCLGAGAGAVYRGINKNGETVAVKVKLSMKLSLSTYKMEIDILKLDHNVKYLK 72
 QY 72 AVEETGSRQKYLIMETCSSGSLSYLED-----PENTFGSEEFVLYLRGVAGNMHRL 127
 DB 73 GSYQTNDS--LCIILEYCENGLSRICKNFKIDENVALYTFQ-----VLQGLLYLH 123
 QY 128 ENGIVHRDIKPGNIMRLVGEQSIYKLSDFGARKLDDKEFVSYYGTEEXLHPDYER 187

DB 124 NCGVHRDRIKGANI--LTTKDG--TIKLADFGVATKINLLEDEH-SVVGSPYMAPEVIE- 177
 QY 188 AVLARKPOKAFQVTV--DLMSIGVTLVHAATGSLPPIPGPRRNKEIAYRITTEKPAQA 245
 DB 178 -----LVGATTASDWSVGVCTIYELLDGPPYYDL-----DPTSA 212
 QY 246 ISGTOKOENGPPLMSYSLPTICRLSMGLONQVPLIANILEVEDKCSGFDQFAETSDI 305
 DB 213 LFRWVADHHPPL-----PSNISAAKSFILM-----CCFQKDPNL 246
 QY 306 LQRTVHVSLPQAVLHVYIHAHNTIAIFLEAVYEQTNTPKHQVLEFGH-PCVLEPS 364
 DB 247 RIKT-----RKLKHVPVIMNQTSKFSKDAIDE---VQKNERVAKESTLTALEPT 294
 QY 365 L-----SAOHIAHTAASSPPLTFMSMSD 387
 DB 295 SNRINPTLHSGROSSYHMPESPPTPIAESPD 325

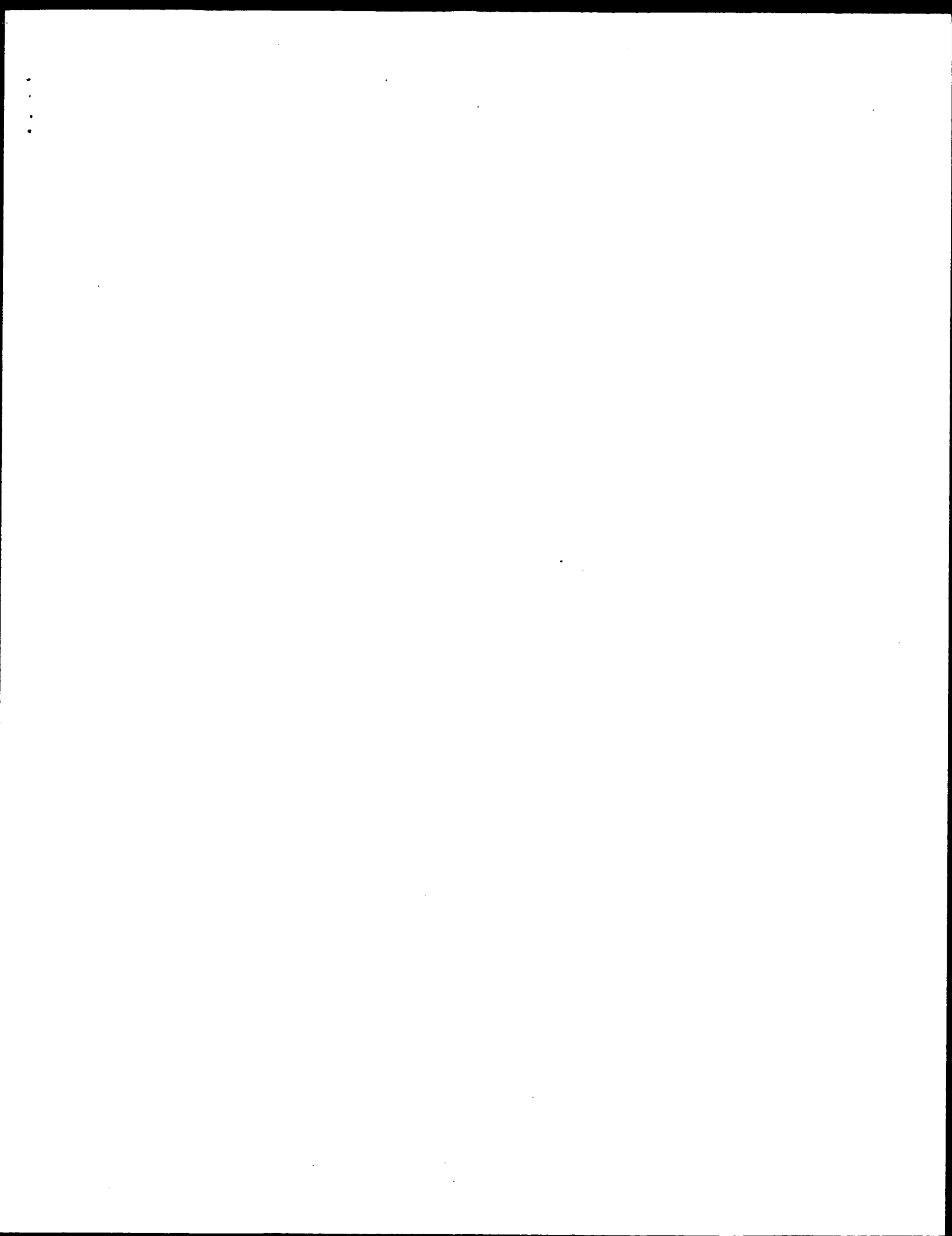
RESULT 15
 DAPK HUMAN STANDARD; PRT; 1431 AA.
 AC P53355;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Death-associated protein kinase 1 (EC 2.7.1.1-) (DAP kinase 1).
 GN DAPK1 OR DAPK.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95129831; PubMed=7828849;
 RA Deiss L.P., Feinstein E., Berissi H., Cohen O., Kinchi A.;
 RT Identification of a novel serine/threonine kinase and a novel 15-kD
 RT protein as potential mediators of the gamma interferon-induced cell
 RT death.";
 RL Genes Dev. 9:15-30(1995).
 RN [2]
 RP REVISIONS TO 164-171.
 RA Feinstein E.;
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
 CC DEATH.
 CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 10 ANK REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X76104; CAA53712.1; -.
 DR HSSP: Q63450; 1A06.
 DR MIM: 600831; -.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00023; ank; 8
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00659; pkinase; 1.
 DR SMART: SM00248; ANK; 7.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 6.

DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50017; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase: Serine/threonine-protein kinase; Calmodulin-binding;
 KW Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
 FT DOMAIN 13 266
 FT DOMAIN 267 334 CALMODULIN-BINDING.
 FT REPEAT 378 407 ANK 1.
 FT REPEAT 411 440 ANK 2.
 FT REPEAT 444 473 ANK 3.
 FT REPEAT 478 507 ANK 4.
 FT REPEAT 511 540 ANK 5.
 FT REPEAT 544 573 ANK 6.
 FT REPEAT 577 606 ANK 7.
 FT REPEAT 610 639 ANK 8.
 FT REPEAT 676 705 ANK 9.
 FT REPEAT 1163 1197 ANK 10.
 FT DOMAIN 1313 1397 DEATH.
 FT NP_BIND 19 27 ATP (BY SIMILARITY).
 FT BINDING 42 42 ATP (BY SIMILARITY).
 FT ACT_SITE 139 139 BY SIMILARITY.
 FT MUTAGEN 42 42 K->A: LOSS OF ACTIVITY.
 SQ SEQUENCE 1431 AA; 160017 MW; 9EB84811004A15B CRC64;

Query Match 7.4%; Score 274; DB 1; Length 1431;
 Best Local Similarity 27.3%; Pred. No. 6.5e-10;
 Matches 88; Conservative 47; Mismatches 105; Indels 82; Gaps 11;

QY 2 OSTTYIIMHTDLDLGGATASVYKRNKSGEVAVKVF--NSASYRR--PREVQVREF 56
 DB 6 QENVDDYDTGELSGQFAVYKCKREKSTGLQYAKFIKKRRYKSSRGVSGHEDIEREV 65
 QY 57 EVYLRINHOIVYKLFVEETGSGROKVLIMEYCSSLISYLEDPENTRGSLFEETLYVL 116
 DB 66 SILKEIÖHPVITLHEVYE--NKTDIVLILELVAGSELDFLAERKS--LTEEATEPL 120
 QY 117 RCYVAGMNLRENGIYHRDIKPGINIRLVGEQSIYKLSDFGAARKLDDEKFEVSVYGT 176
 DB 121 KQILNGVYVYLSQIAHFDLPKPNIMLDRNVPKPIKIIDGLAKIKIDFGNDFKNIFGT 180
 QY 177 EBYLHPDM--YERAVYLRKPOQKAFGVTVDLMSIGVTLVHAATGSLPPIPGPRRNKEIM 234
 DB 181 PERVAPAEIVYE-----PLGLEADWMSIGVITVTLISGASDPL----- 218
 QY 235 YRITTEKPAISGTOKOENGPPLMSYSLPTICRLSMGLONQVPLIANILEVEDKCSG 294
 DB 219 -----GDTKQET-----LANVSAYN-----YE 235
 QY 295 F-DQFFAETS---DLIQRTVI 311
 DB 236 FEDEYFSNTSALAKDFIRLLV 257

Search completed: May 14, 2002, 17:32:11
 Job time: 15324 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 14, 2002, 19:10:07 ; Search time 142.98 Seconds

(without alignments)
867.515 Million cell updates/sec

Title: US-09-582-397a-4

Perfect score: 3726
Sequence: 1 MOSTTNYLMHTDILGGGAT.....IQDNNRLIERLRVPSAPDV 717

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1660	44.6	729	4 Q9UHD2	Q9UHD2 homo sapien
2	1649	44.3	729	11 Q9DC03	Q9DC03 mus musculu
3	1647	44.2	729	11 Q9UHD2	Q9UHD2 mus musculu
4	1146.5	30.8	711	5 Q9VY8	Q9VY8 drosophila
5	428	11.5	756	6 Q9SVK0	Q9SVK0 bos taurus
6	388.5	10.4	731	5 Q9GV6	Q9GV6 drosophila
7	387.5	10.4	741	5 Q9VE25	Q9VE25 drosophila
8	387.5	10.4	751	5 Q9U698	Q9U698 drosophila
9	384.5	10.3	731	5 Q9UJ11	Q9UJ11 drosophila
10	382.5	10.3	731	5 Q9U7F5	Q9U7F5 drosophila
11	364	9.8	732	5 Q61565	Q61565 crassostrea
12	348.5	9.4	740	6 Q9SKV1	Q9SKV1 bos taurus
13	304.5	8.2	1036	4 Q75119	Q75119 homo sapien
14	298	8.0	1090	5 Q9N9J2	Q9N9J2 leishmania
15	294.5	7.9	1037	11 Q9WTP4	Q9WTP4 mus musculu
16	294.5	7.9	1037	11 Q9Y01	Q9Y01 mus musculu

17	293	7.9	1097	10 Q9SX42	Q9SX42 arabidopsis
18	292	7.8	1090	5 Q9GRT3	Q9GRT3 leishmania
19	289	7.8	370	4 Q9UIK4	Q9UIK4 homo sapien
20	288	7.7	370	4 Q75892	Q75892 homo sapien
21	287.5	7.7	1311	4 Q9ULE2	Q9ULE2 homo sapien
22	287.5	7.7	1315	4 Q9NRP7	Q9NRP7 homo sapien
23	287	7.7	1430	11 Q9JUP7	Q9JUP7 mus musculu
24	286.5	7.7	1231	11 Q55092	Q55092 cavia porce
25	286	7.7	370	11 Q9QV44	Q9QV44 mus musculu
26	286	7.7	1049	4 Q94957	Q94957 mus sapien
27	285	7.6	454	4 Q43293	Q43293 homo sapien
28	285	7.6	690	10 Q40541	Q40541 nicotiana t
29	283.5	7.6	520	5 Q9VHF6	Q9VHF6 drosophila
30	283	7.6	1497	5 Q95YH6	Q95YH6 drosophila
31	283	7.6	1571	5 Q95YH7	Q95YH7 drosophila
32	283	7.6	1612	5 Q9VE37	Q9VE37 drosophila
33	280.5	7.5	504	11 Q9QV26	Q9QV26 mus musculu
34	279.5	7.5	483	10 Q9FJ55	Q9FJ55 arabidopsis
35	278	7.5	345	11 Q9CV44	Q9CV44 mus musculu
36	275.5	7.4	478	5 Q62571	Q62571 suberites d
37	275	7.4	448	11 Q54784	Q54784 mus musculu
38	275	7.4	448	11 Q88764	Q88764 rattus norv
39	275	7.4	1039	5 Q9VW68	Q9VW68 drosophila
40	275	7.4	1368	10 Q81809	Q81809 arabidopsis
41	274	7.4	367	4 Q9BTL8	Q9BTL8 homo sapien
42	274	7.4	1368	10 Q9LJD8	Q9LJD8 arabidopsis
43	273.5	7.3	688	4 Q9BYD8	Q9BYD8 homo sapien
44	273	7.3	484	11 Q9QVZ4	Q9QVZ4 mus musculu
45	273	7.3	729	11 Q9JKE4	Q9JKE4 mus musculu

ALIGNMENTS

RESULT	ID	Q9UHD2	PRELIMINARY:	PRT:	729 AA.
AC	Q9UHD2	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	TANK BINDING KINASE TBK1 (NF-KB-ACTIVATING KINASE NAK).				
GN	TBK1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]	SEQUENCE FROM N.A.			
RP	TISSUE=SPLEEN;				
RC	MEDLINE=20050564; PubMed=10581243;				
RA	Pomerantz J.L., Baltimore D.;				
RT	*NF-kB activation by a signaling complex containing TRAF2, TANK, and				
RT	TBK1, a novel IKK-related kinase.*;				
RL	EMBO J. 18:6694-6704(1999).				
RN	[2]	SEQUENCE FROM N.A.			
RP	MEDLINE=20244479; PubMed=10783893;				
RA	Tojima Y., Fujimoto A., Delhase M., Chen Y., Hatakeyama S.,				
RA	Nakayama K., Kaneko Y., Nimura Y., Motoyama N., Ikeda K., Karin M.,				
RA	Nakatsushiki M.;				
RT	*NAK is an IkappaB kinase-activating kinase.*;				
RL	Nature 404:778-782(2000).				
DR	EMBL; AF191838; AAF05989.1; -				
DR	EMBL; AF174536; AAF69106.1; -				
DR	InterPro: IPR000719: Euk.pkinase.				
DR	Pfam: PF00069: pkinase, 1.				
DR	PROSITE: PS00107: PROTEIN_KINASE_ATP, UNKNOWN_1.				
DR	PROSITE: PS0011: PROTEIN_KINASE_DOM, 1.				
KW	ATP-binding; kinase; Transferase.				
SQ	SEQUENCE 729 AA; 83642 MW; B58BAFE1B502276D CRC64;				

Db 479 VKVY-----EKLKAVN--LEAAELGEISDITKLLRLSSSGTIESSLODSSRLSPG 529

Oy 526 G--EELKKNRQIHEDNKSIOKIOCLDKMHFTYKQFKSRMRPGLSYNEQIHLKDKVN 583

Db 530 GLADFWAHGEGHPRDRNVEKLOVLLNCTEITYOFKKKARRRLAYNEQIHKFDKOK 589

Oy 584 FSHLAKRLLOVPOBEVCYQTVSVLTHGKRMROYORONHILHIGSVATCNSEAGAOE 643

Db 590 LYYHAKRKAMSHFSECEYKRAEKFKDSEEMWKRMLHRLKQLSLTMOCCFDEIEEVSRYOD 649

Oy 644 SLNKIFDOLLDRASEGAEVSPQMAP--HPGDP--KDLVFHMOELCNDKMLAFDLQDN 701

Db 650 YTNELQETLQOKMLAASG--VKHAMAPIYSSNTLVEMTLGKKLKEEMGVYKELAE 707

Oy 702 NRIER 707

Db 708 NHILR 713

RESULT 3

Oy 09WUN2 PRELIMINARY; PRT: 729 AA.

AC 09WUN2:

DT 01-NOV-1999 (TREMblrel. 12, Created)

DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)

DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE T2K PROTEIN KINASE HOMOLOG.

GN T2K1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SWISS-WEBSTER/NIH;

RA Wisniewski D., Marcy A.I.;

RT "Mus musculus homolog to human T2K cDNA.";

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=SPLEEN;

RC MEDLINE=20050564; PubMed=10581243;

RA Pomerantz J.L., Baltimore D.;

RT "NF-kB activation by a signaling complex containing TRAF2, TANK, and TRB1, a novel IKK-related kinase.";

RL EMBL J. 18:6694-6704(1999).

DR EMBL; AF145705; AAD34530.1; -

DR EMBL; AF191839; AAF05990.1; -

DR MGD; MGI:1929658; Tdk1.

DR InterPro: IPR000719; Euk_kinase.

DR Pfam: PF00069; Pkinase.1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

RW ATP-binding; kinase; transferase.

SO SEQUENCE 729 AA; 83424 MW; 978ADDE3061DACD1 CRC64;

Query Match 44.2%; Score 1647; DB 11; Length 729;

Best Local Similarity 46.4%; Pred. No. 2.1e-121;

Matches 337; Conservative 129; Mismatches 228; Indels 32; Gaps 8;

Oy 181 HPDMYRAVLARKPOOKAFGVFVNLMSIGVLYHAATGSLPFIPEGPRRKNKEIMYRTTE 240

Db 181 HPDMYRAVLARKPOOKAFGVFVNLMSIGVLYHAATGSLPFIPEGPRRKNKEIMYRTTE 240

Oy 241 KPAAGISGTOKEENGPLEMSYSLPTGRSLMGLONOLVITLANILEVEDKCMGDFQFA 300

Db 241 KPAAGISGTOKEENGPLEMSYSLPTGRSLMGLONOLVITLANILEVEDKCMGDFQFA 300

Oy 301 ETSIDILQRTVIVHFSLPQAVLHVHTYHANTTAIFLENYEDONTVPKHOEYLFEGHCV 360

Db 301 ETSIDILQRTVIVHFSLPQAVLHVHTYHANTTAIFLENYEDONTVPKHOEYLFEGHCV 360

Oy 361 LEPSLSAONIAHTAASSPLTFSMSSDTPKGLAFRDPALDVPKVDLQADYSTAKCV 420

Db 361 LEPSLSAONIAHTAASSPLTFSMSSDTPKGLAFRDPALDVPKVDLQADYSTAKCV 420

Oy 421 LGAGYQALMLARVLDGQALMLRGHMLVEVLADTQCOOTL-----EYRTT 465

Db 421 LGAGYQALMLARVLDGQALMLRGHMLVEVLADTQCOOTL-----EYRTT 465

Oy 466 ALLYLSSLGTERFSSGSGMPDVQERKEATLRTLOTLSLSCSHNTETORSLCL 525

Db 466 ALLYLSSLGTERFSSGSGMPDVQERKEATLRTLOTLSLSCSHNTETORSLCL 525

Oy 479 VKVY-----EKLKAVN--LEAAELGEISDITKLLRLSSSGTIESSLODSSRLSPG 529

Db 479 VKVY-----EKLKAVN--LEAAELGEISDITKLLRLSSSGTIESSLODSSRLSPG 529

Oy 526 G--EELKKNRQIHEDNKSIOKIOCLDKMHFTYKQFKSRMRPGLSYNEQIHLKDKVN 583

Db 526 G--EELKKNRQIHEDNKSIOKIOCLDKMHFTYKQFKSRMRPGLSYNEQIHLKDKVN 583

Oy 530 GLADFWAHGEGHPRDRNVEKLOVLLNCTEITYOFKKKARRRLAYNEQIHKFDKOK 589

Db 530 GLADFWAHGEGHPRDRNVEKLOVLLNCTEITYOFKKKARRRLAYNEQIHKFDKOK 589

Oy 584 FSHLAKRLLOVPOBEVCYQTVSVLTHGKRMROYORONHILHIGSVATCNSEAGAOE 643

Db 584 FSHLAKRLLOVPOBEVCYQTVSVLTHGKRMROYORONHILHIGSVATCNSEAGAOE 643

Oy 590 LYYHAKRKAMSHFSECEYKRAEKFKDSEEMWKRMLHRLKQLSLTMOCCFDEIEEVSRYOD 649

Db 590 LYYHAKRKAMSHFSECEYKRAEKFKDSEEMWKRMLHRLKQLSLTMOCCFDEIEEVSRYOD 649

Oy 644 SLNKIFDOLLDRASEGAEVSPQMAP--HPGDP--KDLVFHMOELCNDKMLAFDLQDN 701

Db 644 SLNKIFDOLLDRASEGAEVSPQMAP--HPGDP--KDLVFHMOELCNDKMLAFDLQDN 701

Oy 650 YTNELQETLQOKMLAASG--VKHAMAPIYSSNTLVEMTLGKKLKEEMGVYKELAE 707

Db 650 YTNELQETLQOKMLAASG--VKHAMAPIYSSNTLVEMTLGKKLKEEMGVYKELAE 707

Oy 702 NRIER 707

Db 708 NHILR 713

RESULT 4

Oy 09VY8 PRELIMINARY; PRT: 711 AA.

AC 09VY8:

DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE I2 PROTEIN.

GN IK2 OR DIK2 OR CG2615.

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis J.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abtill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Berns P.V., Berman B.P., Brinkstein P., Brotler P., Burkova D., Botchan M.R., Bouck J., Brokstein P., Butler E., Cantler A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Modyarty C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RA Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RT Inohara N.;
 RL "Dlk2, Ikk-1 like protein.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003667; AAF53911.1; -;
 DR EMBL: AF197914; AAF04853.1; -;
 DR FLYbase: FBgn0028633; Ik2.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00240; ubiquitin; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 2.
 DR ATP-binding; Kinase; Transferase
 SO SEQUENCE 711 AA; 81091 MW; 406CB82661262860 CRC64;

Query Match 30.8%; Score 1146.5; DB 5; Length 711;
 Best Local Similarity 37.3%; Pred. No. 7.4e-82;
 Matches 256; Conservative 125; Mismatches 238; Indels 67; Gaps 13;
 QY 1 MGSNTNYLHMTDLGCGATASVYKARKKSGEVAVVAVFNSASVRRPREVOVEFEVLAR 60
 DB 4 LKGSVSYWCTTSVVGKATGSGVGVKKTGESVAVKTFNPSYSHMRPADYOMREFEALK 63
 QY 61 RLNHONIVKLFVFEETGSGROKVLIMEYCGSSGLSLVLEDPENTFGLSSEEFVLVLRGVV 120
 DB 64 KVNHNIVKLLAIEDDQGRGVIVYMEICTGSGSLFNILDDPENSGILPEHEFLVLEHLC 123
 QY 121 AGMHLRENGIVHDIKGNIMRLVGEESGYKLSDFGAARKLDDDEKFFSVYGYEYL 180
 DB 124 AGMKHLRBNKIVHDIKGNIMKKTSEGGQTYKLTGGAARLELDNQPFASIGYGYEYL 183
 QY 181 HPDYERAVLRKPOOKAGVTVDLMSIGVTLYHAATGSLPRTIPRGGRPRNKEMIRITTE 240
 DB 184 HPDLIERAVLRKSTORSTAVNDLMSIGVTLYHAATGSLPRTIPRGGRPRNKEMIRITTE 242
 QY 241 KPAAGISGTQKOEKNGPLMSYSLPITCRLSMGLONOLVPTILANTILEVEDCKMGEFOEFA 300
 DB 243 KASGVISGTQKOEKNGPLMSYSLPITCRLSMGLONOLVPTILANTILEVEDCKMGEFOEFA 302
 QY 301 ETSDLQRTVIVHVSFPAVLHNVYIHAHNTIAIFLEAVYEQTNVTPKHQGYEGHPCV 360
 DB 303 ETVTLIRKRVIVHVSFPAVLHNVYIHAHNTIAIFLEAVYEQTNVTPKHQGYEGHPCV 360
 QY 361 LEPSLSAGHIAHTAASSFLTFSSMDTPKGLARDAVDK---FVPAVDLADYSTA 417
 DB 361 LEKVTPTPTI-----DQIFLYSNDNNVY---LPQDLDPKRPVPPVNVSVENDASLA 411

QY 418 KGVLAGVQALMLAVLVDGALMLRGLHWLEVYDTCQOTLEYTR-----TALLYL 470
 DB 412 KACSVGHECKRRRVDFITSMDLILKIGVEHLEMTVTTITLTKTESFNDLSTIDYA 471
 QY 471 GSSLTERFSSSGMPDQERKATELRRLTQTSSEILSKC--SINVTETORSLSCGEE 528
 DB 472 DVVHSMARVTKD-----QETITLTALENKSDPDGADVTSQMKHFPVIDE 520
 QY 529 LKANDQ-----IHF-----DNKSIOKIQCCLDKMFHYKOPKSRMRPGLSYNEQIHL 579
 DB 521 L---NDQWSSMHGKCKCPKTRASAQKYLVERLDSMQHLLRDRATRTLYNDQFHAL 577
 QY 580 DKVNSHLAKRLQYQD-----ECYQTVQSVLTGKRRROYQRAQNHLLIGH 629
 DB 578 EKIKVDHNGKRRKALLDNVNPYQAQIECLADW-----YKLAQVYLLKTOILEK 627
 QY 630 SVATCNSEARGAESLKNKIFDQLDLD 655
 DB 628 DVRCERKLTNGIRDELHYVKSEIKLD 653
 RESULT 5
 Q95KV0 PRELIMINARY; PRT; 756 AA.
 AC Q95KV0;
 DT 01-DEC-2001 (TREMblrel, 19, Created)
 DT 01-DEC-2001 (TREMblrel, 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel, 19, Last annotation update)
 DE IKB KINASE-BETA.
 GN BIKBETA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rottenberg S., Dobbelaere D.A.E., Heusaler V.T.;
 RT "Identification and characterisation of the bovine IKB kinases (IKks)
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ414556; CAC93687.1; -;
 KW Kinase.
 SO SEQUENCE 756 AA; 86647 MW; A072D1561A176E5 CRC64;

Query Match 11.5%; Score 428; DB 6; Length 756;
 Best Local Similarity 22.9%; Pred. No. 5.2e-25;
 Matches 181; Conservative 116; Mismatches 303; Indels 190; Gaps 23;
 QY 9 WHTDGLGCGATASVYKARKKSGEVAVVAVFNSASVRRPREVOVEFEVLARLNQINIV 68
 DB 15 WEMKERLGSTGFGVIVRNHNOETGBOITAICQKQOELSPRRERWCLEIQRNLNPNV 74
 QY 69 KLAVERE-----TGSROKVLIMEYCGSSGLSLVLEDPENTFGLSSEEFVLVLRGVV 124
 DB 75 AARDVPEGMOSLAPNDPLFLAMEYCOGDLRKVLYNFENOCGRALREBALITLSDIASAR 134
 QY 125 HIRENGIVHDIKGNIMRLVGEESGYKLSDFGAARKLDDDEKFFSVYGYEYLHPRM 184
 DB 135 YLHNRIINHDLPENIVLQGGEO-RLIKHITLDLGAKELDGDSLCTSFSTVGLQYLAPEL 193
 QY 185 YERAVLRKPOOKAGVTVDLMSIGVTLYHAATGSLPRTIPRGGRPRNKEMIRITTE 238
 DB 194 LE-----QKTYTVIVDYSFGTALAFECITGFRFLRNQORVOMHSKVRKSEMDIV 245
 QY 239 TEPRPAISGTQKOEKNGPLMSYSLPITCRLSMGLONOLVPTILANTILEVEDCKM 293
 DB 246 SE-----DLGAVKFSGLSPHPNNLSVLAQRLKMLQIMMHNPRQKGTDRY 294
 QY 294 GFDQFAETSDILQRTVIVHVSFPAVLHNVYIHAHNTIAIFLEAVYEQTNVTPKHQGYE 353

Db 295 GPMGCFKALDILINKLHVLMVMTGLHTVPEDEDSIQSLKARTRODTGLEEDQL 354
 Qy 354 FECHPCVLEPSLSAQ-----HIAHTAASSPLTFEMSDTPR----GLAF 394
 Db 355 QEAGLALITDKRAMOCLSDGKINEGRTIDMDLVLEFDSRVITYESQVSPQDPESVSCIL 414
 Qy 395 RDALDVPKRVPRVDQADYSTAKVIGAGYQALMLARVLDDGQALMLRGLHW-VLEVLQ 453
 Db 415 QEKRRMLPFF-----QLRKVAQGVWHISIQALK 441
 Qy 454 DTGQOTLEVTATLLYL---GSSSLGTER-----FSSGSMPDVQERKENT 495
 Db 442 EDCSRLOQGGRAAMMLNRNNSCLSKMNSMASMSOQLAKIDFFETSTOIDEKRYEQT 501
 Qy 496 EL-----RTRQTSLEILSKSHVTEQPS-----LS 523
 Db 502 EFGITSDKLLAWREMAQAVELCGRENEVKHLYERMALQTDIVDQSRPMGRKGGTLD 561
 Qy 524 CLGEBEL-----KNRDOIHEDNKS-----IQKIQCLDKMHPFYKQFKSRMRPQL 569
 Db 562 DLEQANELRYRLREKPRDQRTGDSQEWRLQLAQIGFEKKVRYITYQLSKT-----V 616
 Qy 570 SYNEQOIHKLKDVNFSLAKRLQVFOECVQTYQVSLVTHGKRM--ROYQRAQHNL-HL 626
 Db 617 VCKOKALELPPKV-----EEV-----VSLMSDEKKNVVRLOQEKQOKELML 657
 Qy 627 IGHVATCNSEARGAQSLSKIFDQLLDRASEGAESVQPMAPHPDP---PRDLVE 682
 Db 658 LKINCSYKRGVSGSPDSMN-----ASHLSHPCOLMSQPCPTAPSLFEAAEKSDLYA 710
 Qy 683 HMOELCNMCK 692
 Db 711 EAHFLCTQLE 720
 RESULT 6
 Q9GYV6 PRELIMINARY; PRT; 731 AA.
 AC Q9GYV6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE IKAPPAB KINASE BETA.
 GN IRDS OR IKKBETA OR CG4201.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Silverman N., Zhou R., Stoeven S., Pandey N., Hultmark D.,
 RA Mandatis T.;
 RT "A Drosophila IkappaB kinase complex required for Relish cleavage and
 RT antibacterial immunity."
 RL Genes Dev. 0:0-0(2000).
 CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF294395; AAC02485.1;
 DR FLYBASE: FBgn0024222; Ird5.
 DR InterPro: IPR000719; Euk_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; kinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: P550011; PROTEIN KINASE, DOM; 1.
 DR PROSITE: P550018; PROTEIN KINASE, ST; 1.
 KM ATP-binding, kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 731 AA; 84193 MW; 64386AB0F983BBC6 CMC64;

Query Match 10.4%; Score 388.5; DB 5; Length 731;
 Best Local Similarity 23.6%; Pred. No. 6.6e-22;

Matches 182; Conservative 118; Mismatches 323; Indels 147; Gaps 29;
 Qy 9 MHTDDLLGOGATASYKARKKSGEVAAYKVN-----SASY 45
 Db 21 WERCNRLGEGGFLGVYHMRRTTGRELATKHIKEMALSDQGVKLSERKNELMSQF 80
 Qy 46 RRPE-----VOVEFEVLRRLHONIVKLFVVEETGGSQKQLIMEYCGSSGLSVLEDP 101
 Db 81 KNFPHIYAGVIDEDPDLLEYLNGMFSAKL-----PAYLEYCNGGVRRRLQSP 129
 Qy 102 ENTFTGLSEEEFLVLRVAVGAMNHLEN-GIVHRDIPGNIRMLVGEOSQSYKLSDFGA 160
 Db 130 ENANGLEFEFEVROLGALRKALHFLHSQCGICHRDKPDNVIYQKGVDSKKYIKLDFEL 189
 Qy 161 ARKLDDDEKFEVSYGTEEYLHPMYERAVLRRPQKAFGVTVLMSIGVTLVHAATGSLP 220
 Db 190 ARGTPDQTMQSVGTRHYYAPEVENG-----YNSYDMLSFVYAVHLYTGELP 241
 Qy 221 FIPPGFRNRKELMYRTTEKPRAGALSQV-KQENGLFEMSYSLPTTCLSKMLQNLV- 278
 Db 242 FIPH---QTLKNILNL-IRKPAKCAIATEDPBDNTRFVNQFELPQTHHLSRPMQAQFTK 297
 Qy 279 ----PILANILEVEDKCMGDFDEFAETSDILORTYVHVSFPOAVLHHYIIAHNTIAI 334
 Db 298 WLASPLNSNTERKQOLANVPVYFADLDKILNMNVLTFAVNCNCELEVAASAEMTKMD 357
 Qy 335 FLEAVYEQTNVTPKHOEYLF-EGHPCVLEPSLSAQHIAHTAASSPLTF-----SKSSPT 388
 Db 358 LIALIVLDTGMDKELEYFLPTSHP-----HKTIPKSTPIQLVYEEMSDTSKDS 407
 Qy 389 PKGLAFRDPALDVKFVPKVDQADYSTAKVIGCA-----GYQALML-ARYLLDG 437
 Db 408 RKKTKRSNP--PVMLYIFQVAKCEDYKIPEPILSISRKTIANKFKTEKMLDKRYVLD- 464
 Qy 438 QALMLRGLHWLEVLQDTCCQOTLEVTATLLYL---SSLTERFSSGSGMPDVQERKKA 494
 Db 465 -----MLYVL-----TKQARHEMLVSGINERALSLEDEMENSFIOSID-KQR 507
 Qy 495 TELTRLOTLEILSKSHNVTETQRSLSLCEGELLNRQDIEDNKSIOK-IQCCLDKM 553
 Db 508 IISFAVDQTLSTLKEAQAKIPSRQLISSAQWELNRYNFTIISASISFLEACIREA 567
 Qy 554 HPIYK---QPKSRMRPGLSYNEOIHKLKDVNFSLAKRLQVFOECVQTYQVSLVTH 610
 Db 568 KDMVTTNQLKREYCEKPL-FDCARFYKYLICNGAIISPSPLNDADAEFKS-REFLYNE 625
 Qy 611 GKRMROYRAQNHNLHLLI-----GHSVATCNSEARGAQSLSKIFDQLLDRASEGAESV 666
 Db 626 GE-AHHLPRKSIDHMYLVFKTKRESIPVLQFCIDIKKEIPQINQMILMSASS-----TP 678
 Qy 667 QP-----MARHPGDPKD---LVFHHQ-----LCNMLK 693
 Db 679 PKLELSAMRLAISGSSPSPDPSLRTINAIEAERINNILLVNEKTI 728
 RESULT 7
 Q9VEZ5 PRELIMINARY; PRT; 741 AA.
 AC Q9VEZ5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE IKK PROTEIN.
 GN IRDS OR IKK OR CG4201.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=107196006; PubMed=10731132;

RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaladas P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Chame M., Pfeiffer B.D.,
RA Abiri J.F., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borova D., Botchan M.R., Bouck H., Brockstein P., Brothier P.,
RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chery J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doop L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Foster A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ileguam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Li X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostoslavsky D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard D.R., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrstka R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley R.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF003711; AAF55267.1; -
DR FLYBase: FBgn0024222; lrd5.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 741 AA; 85146 MW; 546616C8F964974B CRC64;

Query Match 10.4%; Score 387.5; DB 5; Length 741;
Best Local Similarity 24.1%; Pred. No. 8.1e-22;
Matches 170; Conservative 95; Mismatches 278; Indels 161; Gaps 25;

QY 9 WHTDILLGCGATATSYKARKKSGEVAAYKFN-----SASY 45
DB 41 WERCNMGEGGFGVLVHMRNRTTGRREIATKRIKEMGALSADDOVKLSERNKNEKLSRPF 100
QY 46 RRPE-----VOVREFEVLRLNHQNIKLVFAVEETGSGROKYLIMEYCGSSGLSVLEDP 101
DB 101 KNFPHIYAGVDIEDPDLLEYLNGMFSAKL-----PVIVLEYCGNGDVRRKLGSP 149
QY 102 ENTGGLSEEEFVLVRCVAVGAMNHLREN-GIVHRDIKPGNIRLVGEESQSYLSIDRCA 160
DB 150 ENANGILTEFEVRQILGALKRALHFLHSGGICHRDLKPNYIYQGVCKKTKIKLDFGL 209
QY 161 AKRLDDEKFEVYVGTGEELVLDHMTERRAVLRKPKQAKGCVTVLWSIGVTLVHAATGSLP 220
DB 210 AKTPQQTWVQSVGTRHYADEVENGPF-----YNSTVDLWSFGVIAVELVTGELP 261
QY 221 FTIPGGRRNKEIMYRITTEKPAAGISGTQ-KQENGPLEMSVSLITCRLSGLONOLV- 278
DB 262 FTRP---QTLKNIILNL-IKRPAKAIATEDPEDNTRFVNOFELPQTHILSRPMAAQFTK 317

QY 279 ----PILANILEVEDKCMGDFQFAETSDIQLQRTIVHFSLPQAVLHYHIAHNTAI 334
DB 318 WLASPLNSNTERKQGLAANNVPVFAFDLKLNNVLTIFAVNCCLEFAVAEAMTKMD 377
QY 335 FLEAVYEQNTVTPKHQYELF-EGHPCVLEPSLSAQHIAHTAASPPLTF-----SNSSDT 388
DB 378 LIALIVDTGDEKELFYVLPESH-----HKTIPKSTPIQLVYEWSDTSKDS 427
QY 389 PKGLAFDPALDYKFEVPKVDLQADYSTAKVICA-----GYQALML-ARVLIDG 437
DB 428 RKTWRKSNP--PVMLYIFQVKKEDDYKIPPIILISRKTIANKFKTERKWLQKRVLD- 484
QY 438 QALMLRQLHMYLEVLYDTCQOTLEVTALLYLGG---SSIGTERFSSGMPDVERKPA 494
DB 485 -----MLVYL-----TKQARYEWLVGINERALSLDEDMENSFIDSID-KOR 527
QY 495 TELRTRQLTSELISKSHVETQSLSLGSELKKNRQIHEDNKSTQK-IQCCL--- 550
DB 528 IITSFATDQLTSLKEAQAKIPSRQLISSQWKEKLNRYNFIQSASIRSFLEACLRBA 587
QY 551 -----DKMHFTYK-----QFKSRMRPGLSYN 572
DB 588 KDWKTTNQLRKVECEKDLFCARFYKTYLCNCAIISPSELNNDAAEFKSRK---LYN 644
QY 573 EEQIHL-----DKVNSHLAKR-----LIQVQECVQTYOVS 607
DB 645 EGRARHLPSIDHMYLFEKTKESIPVLLQGFQDIIKEIFQINTL 688

RESULT 8
QY 090698 PRELIMINARY; PRT; 751 AA.
AC 090698:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE IKK-LIKE PROTEIN.
GN IRDS OR CG4201.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Inohara N., Nunez G.;
RT "DIR, a IKK-like protein of *Drosophila*,"
Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
RL EMBL: AF190636; AAF04130.1; -
DR FLYBase: FBgn0024222; lrd5.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 751 AA; 86344 MW; 0060CEFA4BCB30A CRC64;

Query Match 10.4%; Score 387.5; DB 5; Length 751;
Best Local Similarity 23.9%; Pred. No. 8.2e-22;
Matches 184; Conservative 117; Mismatches 322; Indels 147; Gaps 30;

QY 9 WHTDILLGCGATATSYKARKKSGEVAAYKFN-----SASY 45
DB 41 WERCNMGEGGFGVLVHMRNRTTGRREIATKRIKEMGALSADDOVKLSERNKNEKLSRPF 100
QY 46 RRPE-----VOVREFEVLRLNHQNIKLVFAVEETGSGROKYLIMEYCGSSGLSVLEDP 101
DB 101 KNFPHIYAGVDIEDPDLLEYLNGMFSAKL-----PVIVLEYCGNGDVRRKLGSP 149

DE CACTUS KINASE IKK.
 GN IRD5 OR CG4201.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Medzhilov R.M., Janeway C.J.;
 RT "Cloning and characterization of the Drosophila cactus kinase."
 RT Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF128403; AAF04346.1; .
 DR Flybase: FBgn0024222; Ird5.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 731 AA; 84157 MW; 15381A6AD1EB343 CRC64;
 SQ

Query Match 10.3%; Score 382.5; DB 5; Length 731;
 Best Local Similarity 23.3%; Pred. No. 2e-21;
 Matches 162; Conservative 114; Mismatches 276; Indels 143; Gaps 25;

OY 9 WHTDDLGGATATSYKARKKSGEVAVKFN-----SASY 45
 DB 21 WERCNLLGGGGLYIHRNRRTGRELTKHKEMGALSADQVKLSRKNKELNWSKOF 80
 OY 46 RRPPE-----VOYREFEVRLNHNQIVKFAVEETGSRQKVLMEYSSGSLSLVEDP 101
 DB 81 KNEPHIVAGVLEDEDFLEYLNGMFSAKL-----PVIVLEYCNGGDVRRKRLQSP 129
 OY 102 ENTFELISEEFLVLRGVAGNMHLREN-GIVHRDIPKPNIMRLVGEESGSIYKLSDPGA 160
 DB 130 ENANLTFEYERQIIGALKRKALHFLHSOGGICHRDLKDNKNTVIGRGVKKIYKLTDEGL 189
 OY 161 ARKLDDKEFVSVYGTETEYLHPDMYTERAVLRKPOOKAGVTVDLMSLGVTLYHAATGSLP 220
 DB 190 ARGPDQDMVQSVGTFRHYVAPEVENGF-----YNSIVDLMSPEVIVAYELVTGELP 241
 OY 221 FIFEGSPRNKEIMYRITTEKPAALISTQ-KOENGPLEMSYSLPTCRLSMGLQNDLV 278
 DB 242 FIFP-----OTLKNITLNL-IKRPACIATEDPEDNTRFVNQFELPQTHLSRPWAAQFTK 297
 OY 279 ----PILANILEVEDKCMGFDFEAETSDILOFTVIVHVSFLPQAVLHHVYTHAHTIAI 334
 DB 298 WLASPLNSYKERGQLANNVPVAFADDKILNNVLTIFAVNCCERLEIVASLAKMTKD 357
 OY 335 FLEAVYEQTNPVKHOELF-EGHPCVLEPSLSKQIHNAHTAASPFLF-----SMSDT 388
 DB 358 LIALIVLDGDEKELFYVLPISHP-----HKTIPTKSPPLQYVEMSDTSKDS 407
 OY 389 PKGLAFRPAADVKEFVKVLDADYSTAKGVLA-----GYQALML-ARVLID- 436
 DB 408 RKKTKRNSP--PVMLYIYQVAKCEDYKIPEDILSLSRKLTANKFKTERLQKRVYIDM 465
 OY 437 -----GOALML-----RGLHMLVLEVDTCQOTLEVTALILYSSLSIGTERSSG 482
 DB 466 LYLTLKEQARYEMLVSGINERALSLEDEMENSFIDSIDKRIITISAYDOL-----T 518
 OY 483 SGMDVQERKATELRRLQTLSTLSKSHNTETORSL-----SCIGE--ELLNKRDQ 535
 DB 519 SILLEAQAQSPSRQLISSAQW--EKLNNRNYNFIIOAKSIRSFLACLREAKDKVKTNQ 576
 OY 536 IHNENKSIQKIQCL-----DKMHTYQKFKSKRRPCLSTNEQIHKL-- 579
 DB 577 LRKEVCEKDLFDCAEFYKKYLCNCAIISPSELNDAEFAKSRPK--LYNEGEARHLPK 633
 OY 580 --DKVNFSLAKR-----LIQVFEQECVQTYOVS 607

DB 634 SIDHMYLYEFTKKSIPVLLQOFDIDKEIFQINL 668

RESULT 11
 ID 061565 PRELIMINARY; PRT; 732 AA.
 AC 061565;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE 1-KAPPA-B KINASE.
 GN IKK.
 OS Crassostrea gigas (Pacific oyster).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
 OC Ostreoida; Ostreidae; Crassostrea.
 NCBI_TaxID=29159;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99332074; PubMed=10405163;
 RA Escoubas J.M., Briant L., Montagnani C., Hez S., Devaux C., Roch P.;
 RT "Oyster IKK-like protein shares structural and functional properties
 RT with its mammalian homologues."
 RL FEBS Lett. 453:293-298(1999).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF051320; AAC05683.1; .
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 732 AA; 84215 MW; 871EB8D1CA3E39AF CRC64;
 SQ

Query Match 9.8%; Score 364; DB 5; Length 732;
 Best Local Similarity 21.8%; Pred. No. 5.7e-20;
 Matches 169; Conservative 126; Mismatches 321; Indels 158; Gaps 30;

OY 9 WHTDDLGGATATSYKARKKSGEVAVKFN-----FNSASTRRPEVQYREFEVRLNHNQ 66
 DB 12 WIEKILGSGGFCQVYLMKHESRDLTKCKVQSEMMQKHNERTLTVIDIMKRLDHN 71
 OY 67 IVKLFAYE-----ETGSGKOKVLMEYSSGSLSLVEDPENTGSLSEEFVLVLRGVAGM 123
 DB 72 VIAKDVPEPLNVHVGEMPELAMEYSSGDLRKVLKPKENCYGLKQYDRLCYRLIASAV 131
 OY 124 NHLRENGIVARDLKPGNINRLVGEESGSIYKLSDFCAARKLDDKEFVSVYGTETYLHPD 183
 DB 132 EYLAKKRILHRDLKPNIV-LHPTEBOYVYKYVIDLGYAKELDQSSMCTSFVTMOYLAPE 190
 OY 184 MYERAVLRKPOOKAGVTVDLMSLGVTLYHAATGSLPFIPEGSP--RRNKEIMYRITTEK 242
 DB 191 LF-----ASQKYCTVDYMSFGIVFECLTGFPEPLPHVPYTWHEVY-----OKS 237
 OY 243 AGAISTQKQENPLEMSYSLPTCRLSMGLQNDLVPIANILEVEDKCM----- 293
 DB 238 QDDITGFYNSD-GEVFEFSQKILPTHLCRSMQAYFEQWLSMLR-----WQSRLGGGR 290
 OY 294 -GPDQFAETSDILOFTVIVHVSFLPQAVLHHVYTHAHTIAIFLAAYEQTNVTPKHQY 352
 DB 291 DGRPHCFRVLDTMLNVKILHILYVPCNLLSYPLVENSIOELQRIEKETGVKVEDDI 350
 OY 353 LFEHGHCVLEPSLSKQIHNAHTAASP--LTLESMSSDTPKGL-----AFNDP 397
 DB 351 LLASGSP--DPLNIGA-HQCTWAPGGEEDVAVFLFAAGEGNGGSGIQKPLPTNVQGIKPEP 408
 OY 398 ALDVPKEFVKVLDADYSTAKGVLAGYQALMLAVLLDGLQALMLRGL----- 445
 DB 409 TIVLPFOQK-----KAAEAAYVQCNOQYVDFRRLIQSQRAAMLSMLRTHNDFAKREKK 462
 OY 446 -----HWV--LEVIDTQOTLEVTALILYSSLSIGTERSSGSGMDV-----Q 489

Db 463 MVSCEHLVSKLDYFEEDLOHLE-----LY-----GIOSRDGISAHEVAKMKVGE 511
 QY 490 ERKEATELRLQTLSEILSKSHNTETORS--LSCLDELLKNDQI----- 536
 Db 512 EMKLYSHLEWOTLHQOSLALQTKLELOKSEFARKOHEVLENLSEIAKCTELYOEM 571
 QY 537 -----HEDNKSIOK--IQCCLDK--MHFIYKOFK-----SRMPGLSYNE 573
 Db 572 RQAGKGRREYKHKRMKMYLVKVCIFTRQOSLODLTLHGKICACKHELFOLLPSIQOR 631
 QY 574 EOIHKLKDNFSLHAKRLLOVEECVQYQVSLYTHGRMROYORAQNH-----LHLIG- 628
 Db 632 EOI-----DETQRLLOAHKROSEIWSLWQMAEG--MARQDSRSGSHASMLSMYG 682
 QY 629 ---HSVATCNSEARGAESLNFEDOL--LDRASQGAESVSPQAPRIPGPP 677
 Db 683 ASLDSTKCDN---RETVQKCDMDIKSLIDHEHELLSMDWSFLPPEKSE 732

RESULT 12

Q95KV1 PRELIMINARY; PRT: 740 AA.
 AC 095KV1;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE IKB_KINASE-ALPHA.
 GN BIKKALPHA.
 OS Bos laurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 OX NCBI_TaxId=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
 RT "Identification and characterisation of the bovine Ikb kinases (IKks)
 RT alpha, beta and gamma."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ414555; CAC93686.1; -
 KW Kinase.
 SQ SEQUENCE 740 AA; 84343 MW; 01903BELLF44D176 CRC64;

Query Match 9.4%; Score 348.5; DB 6; Length 740;

Best Local Similarity 22.2%; Pred. No. 9.8e-19;

Matches 176; Conservative 122; Mismatches 322; Indels 173; Gaps 34;

QY 9 WHTDDLGGATASVYKARKKSGEVAVKVFNSASYRRPEVOVREFVLRRLNHNQIV 68
 Db 15 WEMHERLGTGFGFVNCYLQHRDLKAIKSCRELSTKRRERMCHEIDIMKKNHANV 74
 QY 69 KLRVETG---SRQVLLMEYSSSLSVLEDPENTGSEELVYLRGVAGMNH 125
 Db 75 KACVPELFLINDVFLAMEYCSGGDLKLNKPCCGLESQSLSLSDIGSIRY 134
 QY 126 LRENGIYHRDIPNIRLVGEESQYKLSDFGAARKLDDDEFVSVTEELPHDMY 185
 Db 135 LHEKTIHRLKPNITV-LDDVGGKIMKTIIDGYAKDVQSGISCTFVTLQIADL 193
 QY 186 ERAVLRRPQAKAGVTVLMSIGVTLVHAATGSLPFI---PFGPRRKEIMYRITTEK 241
 Db 194 E-----NKPATATVDVMSFGMVCEAGYRPFLLHNLQPFWMHEKIK-----KK 237
 QY 242 PAGNISTGQENGLRMSVSLP---ITCRLSMGLQVLPILAN-----LLEVE 288
 Db 238 DPKCTFACEEN-TEGVFSSHLRPNLSCLIVPEPMENMLQMLMNDP JORGGPVDLTK 296
 QY 289 EDKCMGFDOFAETSILQRTVIVHVSILPOAVLHNHVIHANHTAILEAVYEQTNTPK 348
 Db 297 QPRC-----FVLMIDLNLKIYHILMTSAKISIFLLPDESLSQSNIERRTGINTG 350
 QY 349 HOEYLF-----GHPVCVLEPSLSAQHI-----AHTAASPLTLFMSSDTPKG 391

Db 351 SEELLSEMGISLDPRKPAQCVLDGVRGDSYMYVLFPSKSTVYGPAPASRLSDCV--N 408
 QY 392 LAFRPAIDVPEF-VPKV-----DLQADYSTAKVGLAGVQALMLARVLDDG-AL 440
 Db 409 YIVODSKTLOPLTIOLRKWAEAHVYSGLEKEDYSR-----LEFGORAA 451
 QY 441 MLRGLHM--VLFLVLDTCQOTLEVRTALLYGSS--LTERFSSGSGMPDVEKKEATE 496
 Db 452 MSLRLRYNTNLTKMNTLISASQKAKLEFFPKSIQDLDEY-----EQTYGIS 503
 QY 497 LTRLOTLSILSKSHNTEFORSLSCIGELLKNRQIHEDNKS-----IQKI- 546
 Db 504 SEKMILKAMKEMEKAIHYA--EVGVIGYLEDQIMSLHTEIMELQKSPYGRROGDLMESE 561
 QY 547 OCCLDKMHFIYKOFKSRMRPG-LSYNEQ-----IHLD-----KYNESHAKRL- 591
 Db 562 ORAID---LYROLKH---RPSDHSYSTENWKIIVTVQSDRYALEFGLSKLGLC 614
 QY 592 -----LQFQBEVQYQVSLVTHGRMROYORAQNHLLHIGSVATCNSEARG- 640
 Db 615 KOKITDLPRKEMALSNKEADSTVFMGKRKKEI-----WHLL--KIACQSSASL 666
 QY 641 ADESILNKIPDOJ--LDRASQGAESVSPQAPRIPGPKDLYRMOELCNDKRL--- 694
 Db 667 VGSLSLEGVTPOLPPTPSAREHNLSCVTPQ-----DGETLAQWIEENLNCGLSTI 718
 QY 695 ---AFDLQNNRL 704
 Db 719 IHEANEGQNNNM 731

RESULT 13

Q75119 PRELIMINARY; PRT: 1036 AA.
 AC 075119;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
 DE KIA0623 PROTEIN.
 GN KIA0623.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro."
 RL DNA Res. 5:169-176(1998).
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB014523; BAA31598.1; -
 DR HSSP: P24941; ICRP.
 DR InterPro: IPR000719; Euk.pkinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase.1.
 DR SMART: SM00220; S_TKC.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1036 AA; 112779 MW; CF73145EF37E641C CRC64;

Query Match 8.2%; Score 304.5; DB 4; Length 1036;

Best Local Similarity 27.0%; Pred. No. 5e-15;

Matches 90; Conservative 59; Mismatches 127; Indels 57; Gaps 11;

QY 1 MOSTYVYLMHTDLDLGGATASVYKARK-KSGEVAVKVFNSASVRRPEVQVREFEVL 59
 Db 1 MEVVGDFEYSKRDVGHGFAVAFVFRGRHROKTDWEVAIKSINKKMLKSQILLGKEIKIL 60
 QY 60 RRLNHNQIKLVFAVEETGSRQKVLIMEYCGSSGLSVLEDPENTFGISEEFLVLRKV 119
 Db 61 KELOHENTIALVDQVLEPNS--VFIMVEYCGNGDLADYLQ-AKGT--ISEDTIRFVLEHOI 115
 QY 120 VAGMNLHRENGIVHRDIKPGNIMRLVGEQSGSI-----YKLSDFGAARLDDEKFAVSY 174
 Db 116 AAMRLHSKGIHHRDLKQNLILSYANRRKSSVSGIRIKIADIEFARYLHNMMAATLC 175
 QY 175 GTEELIHPMTEKRAVLKPKQKAFGVYDLSIGVLYHAATGSLPFIIPGPR----- 228
 Db 176 GSPMVAPEVI-----MSQHYDAKADLMSIGVLYQCLVKGPPF-QANSPODLRFVY 226
 QY 229 -ENKEIMYRITTEKP-----AGASIGTOKO-----ENPLEMYSYLPF-- 265
 Db 227 EKNRSLMSPREPETSPLYANLLGLQNRQKDRMDEAFESHFLEGGPVKKSCEVPVM 286
 QY 266 -----TCRLSMGLQNLVPIIANILEVED 290
 Db 287 YSGSVSGSCSSPSCRFASPPSLPDMQHOIDE 319

RESULT 14

Q9N9J2 PRELIMINARY; PRT; 1090 AA.
 AC 09N9J2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SERINE-THREONINE PROTEIN KINASE (SERINE-THREONINE PROTEIN KINASE MK22).
 GN L6293.02.
 OS Leishmania major.
 OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Aert R., Volckaert G., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Aert R., Volckaert G., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
 RL "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Aert R., Volckaert G., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AL359777; CAB95259.1; -
 DR EMBL: AL359683; CAC37137.1; -
 DR HSSP: P24941; 1CKP.
 DR InterPro: IPR000225; Armadillo.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_Thr_Pkinase.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKC.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.

KW ARP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1090 AA; 121194 MW; 763220306A030B82 CRC64;

Query Match

Best Local Similarity 8.0%; Score 298; DB 5; Length 1090;
 Matches 75; Conservative 39; Mismatches 75; Indels 20; Gaps 8;

QY 15 LGGATASVYKARKKSGEVAVKVFNSASVRRPEVQVREFEVLRLNHNQIKLVFAV 73
 Db 14 IGEISFGRYKARKIGQIVAMKFIYKGRKEKLNKRSLEILTKLHNPHTIMLFDS 73
 QY 74 EETGSRQKVLIMEYCGSSGLSVLEDPENTFGISEEFLVLRGVAGNHRRENGIYH 133
 Db 74 FET--DSDFFVVMYX-AQGLYDILEKO---LPEKVKIKQLQALNLYHSRRIIH 127
 QY 134 RDIKPGNIMRLVGEQSGSIYKLSDFGAARKLD-DDEKFSVYGTETELHPMTEKRAVLK 192
 Db 128 RDMKPNQI--LIGQNG--AVKLADFGFARMSYNTIVLSIKGTPLYMAPELV----- 176
 QY 193 PQOKAFGVYDLSIGVLYHAATGSLPF 221
 Db 177 -QERAYDNVDLMSLGCLYELVYGRPF 204

RESULT 15

Q9WTP4 PRELIMINARY; PRT; 1037 AA.
 AC 09WTP4;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE UNC-51-LIKE KINASE (ULK2).
 GN ULK2 OR ULK2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20027371; PubMed=10557072;
 RA Yan J., Kuroyanagi H., Tomemori T., Okazaki N., Asato K., Matsuda Y., Suzuki Y., Ohshima Y., Mitani S., Masuko Y., Shirasawa T., Muramatsu M.;
 RL "Mouse ULK2, a novel member of the UNC-51-like protein kinases: unique features of functional domains."; Oncogene 18:5850-5859(1999).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB019577; BAAT7341.1; -
 DR HSSP: P24941; 1CKP.
 DR MGD: MGI:1352758; ULK2.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_Thr_Pkinase.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKC.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1037 AA; 112863 MW; D28E11B0B87E9613 CRC64;

Query Match 7.9%; Score 294.5; DB 11; Length 1037;
 Best Local Similarity 27.4%; Pred. No. 3,1e-14;

Matches 88; Conservative 55; Mismatches 121; Indels 57; Gaps 11;

QY 13 DLGGATASVYKARKK-KSGEVAVKVFNSASVRRPEVQVREFEVLRLNHNQIKLV 71
 Db 13 DLVGHGAFVAFVFRGRHROKTDWEVAIKSINKKMLKSQILLGKEIKILOHENTIALV 72
 QY 72 AVEETGSRQKVLIMEYCGSSGLSVLEDPENTFGISEEFLVLRGVAGNHRRENGI 131

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Db 73 DVOELPNS--VFLVMEYCNGLADYLO-AKGT--LSEDTIRVFLHOIAAARILHSKGI 127
QY 132 VHRD.KPGNIMRLVGEEOGS-----IYKLSDEGAARKLDDDEKFEVSYGTEEYLHPDME 186
Db 128 IHRDLKPONILSLVANNRRKSNVSGIRIKIADPGFAKYLHSNTMAATLCGSPMYMAPEYL- 186
QY 187 RAVLRKPOOKAFGVVVDLMSIGVTLYHAATGSLPEIPFGGPR-----RNKEIMYRIYT 239
Db 187 -----KSGHYDAKADLMSIGTVYQCLYKRPF-QANSPODLNMFYEKNRSLMPSIPR 238
QY 240 EKP-----AGAISTOKO-----ENGPLEWYSYSLPI-----TCRL 269
Db 239 ETSPLYLANLLGLORNOCKDRMDFAFESHPRLEQVPVKSCPCVPVYSGPVGSSCSS 298
QY 270 SMGLONQVPIILANTIEVEED 290
Db 299 SPSCRFASPPSLPDMOHIOEE 319
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Search completed: May 14, 2002, 19:10:13
Job time: 5880 sec

